

## HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

### Cross Reference to Related Applications

This application claims priority to the following provisional applications: U.S. Ser. No. 60/188,914, filed March 13, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/192,033, filed March 24, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/198,474, filed April 12, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENE ENCODING THE SAME to Zozulya; U.S. Ser. No. 60/199,335, filed April 24, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/207,702, filed May 26, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/213,849, filed June 23, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/226,534, filed August 16, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/230,732, filed September 7, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; and U.S. Ser. No. 60/266,862, filed February 7, 2001, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya. All of these applications are herein incorporated by reference in their entireties.

### Field of the Invention

The invention relates to newly identified mammalian chemosensory G protein-coupled receptors, particularly olfactory receptors, fragments thereof, classes of such receptors, genes and cDNAs encoding said receptors, vectors including said receptors, and cells that express said receptors. The invention also relates to methods of using such receptors, fragments, genes, cDNAs, vectors, and cells to identify molecules involved in olfactory perception. The invention therefore has application in the selection and design of odorant compositions, as well as malodor blockers (olfactory receptor antagonists), particularly perfumes and fragrance compositions and components of deodorants and other malodor blocking compositions.

### Description of the Related Art

The olfactory system provides sensory information about the chemical composition of the external world. Olfactory sensation is thought to involve distinct signaling pathways. These pathways are believed to be mediated by olfactory receptors (ORs). Cells which express olfactory receptors, when exposed to certain chemical stimuli, elicit olfactory sensation by depolarizing to generate an action potential, which is believed to trigger the sensation.

As such, olfactory receptors specifically recognize molecules that elicit specific olfactory sensation. These molecules are also referred to herein as "odorants." Olfactory receptors belong to the 7-transmembrane receptor superfamily (Buck *et al.*, *Cell* 65:175-87 (1991)), which are also known as G protein-coupled receptors (GPCRs). G protein-coupled receptors control many physiological functions, such as endocrine function, exocrine function, heart rate, lipolysis, carbohydrate metabolism, and transmembrane signaling. The biochemical analysis and molecular cloning of a number of such receptors has revealed many basic principles regarding the function of these receptors.

For example, U. S. Patent No. 5,691,188 describes how upon a ligand binding to a GPCR, the receptor presumably undergoes a conformational change leading to activation of the G protein. G proteins are comprised of three subunits: a guanyl nucleotide binding  $\alpha$  subunit, a  $\beta$  subunit, and a  $\gamma$  subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the  $\alpha$  subunit. When GDP is bound, the G protein exists as a heterotrimer: the  $G\alpha\beta\gamma$  complex. When GTP is bound, the  $\alpha$  subunit dissociates from the heterotrimer, leaving a  $G\beta\gamma$  complex. When a  $G\alpha\beta\gamma$  complex operatively associates with an activated G protein-coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of dissociation of the bound  $G\alpha$  subunit from the  $G\alpha\beta\gamma$  complex increases. The free  $G\alpha$  subunit and  $G\beta\gamma$  complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell.

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel, *Sci. Amer.*, 273:154-59 (1995)). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer, *Semin. Cell Biol.*, 5:25-32 (1994)). The human genome contains approximately one thousand genes that encode a diverse repertoire of olfactory receptors (Rouquier, *Nat. Genet.*, 18:243-50 (1998); Trask, *Hum. Mol. Genet.*, 7:2007-20 (1998)). It has been demonstrated that members of the OR gene family are distributed on all but a few human chromosomes. Through fluorescence *in situ* hybridization analysis, Rouquier showed that OR sequences reside at more than 25 locations in the human genome. Rouquier also determined that the human genome has accumulated a striking number of dysfunctional OR copies: 72% of the analyzed sequences were found to be pseudogenes. An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that chemosensory receptors belong to a multigene family with over a thousand members. For instance, there are up to 1,000 odorant receptors in mammals.

Moreover, each chemosensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses. To analyze odorant-receptor interactions and their effects on olfactory cells, specific ligands and the olfactory receptors to which they bind are identified. This analysis requires isolation and expression of olfactory polypeptides, followed by binding assays.

Some studies suggest that OR genes can be expressed in tissues other than the olfactory epithelium, indicating potential alternative biological roles for this class of chemosensory receptors. Expression of various ORs has been reported in human and murine erythroid cells (Feingold 1999), developing rat heart (Drutel, *Receptor Channels*, 3(1):33-40 (1995)), avian notochord (Nef, *PNAS*, 94(9):4766-71 (1997)) and lingual epithelium (Abe, *FES Lett.*, 316(3):253-56 (1993)). One experimentally documented case also established the existence of a large subset of mammalian ORs transcribed in testes and expressed on the surface of mature spermatozoa, thereby

suggesting a possible role of ORs in sperm chemotaxis (Parmenthler, *Nature*, 355:453-55 (1992); Walensky, *Mol. Med.*, 1(2):130-41 (1998); Branscomb, *Genetics*, 156(2):785-97 (2000)). It was also hypothesized that olfactory receptors might provide molecular codes for highly specific cell-cell recognition functions in development and embryogenesis (Dreyer, *PNAS*, 95(11):9072-77 (1998)).

Complete or partial sequences of numerous human and other eukaryotic chemosensory receptors are currently known. See, e.g., Pilpel, Y. and Lancet, D., *Protein Science*, 8:969-77 (1999); Mombaerts, P., *Annu. Rev. Neurosci.*, 22:487-50 (1999); see also, EP0867508A2, US 5874243, WO 92/17585, WO 95/18140, WO 97/17444, WO 99/67282. Due to the complexity of ligand-receptor interactions, and more particularly odorant-receptor interactions, information about ligand-receptor recognition is lacking. In part, the present invention addresses the need for better understanding of these interactions. The present invention also provides, among other things, novel chemosensory receptors, and methods for utilizing such novel chemosensory receptors and the genes and cDNAs encoding such receptors, especially for identifying compounds that can be used to module chemosensory transduction, such as olfaction.

#### Summary of the Invention

Toward that end, it is an object of the invention to provide a new family of G protein-coupled receptors comprising over two hundred fifty olfactory G protein-coupled receptors (OR) active in olfactory perception. It is another object of the invention to provide fragments and variants of such ORs which retain odorant-binding activity.

It is yet another object of the invention to provide nucleic acid sequences or molecules that encode such ORs, fragments, or allelic variants.

It is still another object of the invention to provide expression vectors which include nucleic acid sequences that encode such ORs, or fragments, or variants thereof, which are operably linked to at least one regulatory sequence such as a promoter, enhancer, or other sequences involved in positive or negative gene transcription and/or translation.

It is still another object of the invention to provide human or non-human cells that functionally express at least one of such ORs, or fragments, or variants thereof.



It is still another object of the invention to provide OR fusion proteins or polypeptides which include at least a fragment of at least one of such ORs.

It is another object of the invention to provide an isolated nucleic acid molecule encoding an OR comprising a nucleic acid sequence that is at least 30%,  
5 more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from the group consisting of: SEQ. ID. NO. 2, SEQ. ID. NO. 4, SEQ. ID. NO. 6, SEQ. ID. NO. 8, SEQ. ID. NO. 10, SEQ. ID. NO. 12, SEQ. ID. NO. 14, SEQ. ID. NO. 16, SEQ. ID. NO. 18, SEQ. ID. NO. 20, SEQ. ID. NO. 22, SEQ. ID. NO. 24, SEQ. ID. NO. 26, SEQ. ID. NO. 28, SEQ. ID. NO. 30, SEQ. ID. NO. 32, SEQ. ID. NO. 34, SEQ. ID. NO. 36, SEQ. ID. NO. 38, SEQ. ID. NO. 40, SEQ. ID. NO. 42, SEQ. ID. NO. 44, SEQ. ID. NO. 46, SEQ. ID. NO. 48, SEQ. ID. NO. 50, SEQ. ID. NO. 52, SEQ. ID. NO. 54, SEQ. ID. NO. 56, SEQ. ID. NO. 58, SEQ. ID. NO. 60, SEQ. ID. NO. 62, SEQ. ID. NO. 64, SEQ. ID. NO. 66, SEQ. ID. NO. 68, SEQ. ID. NO. 70, SEQ. ID. NO. 72, SEQ. ID. NO. 74, SEQ. ID. NO. 76, SEQ. ID. NO. 78, SEQ. ID. NO. 80, SEQ. ID. NO. 82, SEQ. ID. NO. 84, SEQ. ID. NO. 86, SEQ. ID. NO. 88, SEQ. ID. NO. 90, SEQ. ID. NO. 92, SEQ. ID. NO. 94, SEQ. ID. NO. 96, SEQ. ID. NO. 98, SEQ. ID. NO. 100, SEQ. ID. NO. 102, SEQ. ID. NO. 104, SEQ. ID. NO. 106, SEQ. ID. NO. 108, SEQ. ID. NO. 110, SEQ. ID. NO. 112, SEQ. ID. NO. 114, SEQ. ID. NO. 116, SEQ. ID. NO. 118, SEQ. ID. NO. 120, SEQ. ID. NO. 122, SEQ. ID. NO. 124, SEQ. ID. NO. 126, SEQ. ID. NO. 128, SEQ. ID. NO. 130, SEQ. ID. NO. 132, SEQ. ID. NO. 134, SEQ. ID. NO. 136, SEQ. ID. NO. 138, SEQ. ID. NO. 140, SEQ. ID. NO. 142, SEQ. ID. NO. 144, SEQ. ID. NO. 146, SEQ. ID. NO. 148, SEQ. ID. NO. 150, SEQ. ID. NO. 152, SEQ. ID. NO. 154, SEQ. ID. NO. 156, SEQ. ID. NO. 158, SEQ. ID. NO. 160, SEQ. ID. NO. 162, SEQ. ID. NO. 164, SEQ. ID. NO. 166, SEQ. ID. NO. 168, SEQ. ID. NO. 170, SEQ. ID. NO. 172, SEQ. ID. NO. 174, SEQ. ID. NO. 176, SEQ. ID. NO. 178, SEQ. ID. NO. 180, SEQ. ID. NO. 182, SEQ. ID. NO. 184, SEQ. ID. NO. 186, SEQ. ID. NO. 188, SEQ. ID. NO. 190, SEQ. ID. NO. 192, SEQ. ID. NO. 194, SEQ. ID. NO. 196, SEQ. ID. NO. 198, SEQ. ID. NO. 200, SEQ. ID. NO. 202, SEQ. ID. NO. 204, SEQ. ID. NO. 206, SEQ. ID. NO. 208, SEQ. ID. NO. 210, SEQ. ID. NO. 212, SEQ. ID. NO. 214, SEQ. ID. NO. 216, SEQ. ID. NO. 218, SEQ. ID. NO. 220, SEQ. ID. NO. 222, SEQ. ID.

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NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512.

It is a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence which is at least 40%, more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.

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ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251, SEQ. ID. NO. 253,

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 5 SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ. ID. NO. 295, SEQ.  
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 10 ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID. NO. 337, SEQ. ID.  
 NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO. 345, SEQ. ID. NO.  
 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353, SEQ. ID. NO. 355,  
 SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ. ID. NO. 363, SEQ.  
 ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO: 371, SEQ. ID. NO.  
 15 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379, SEQ. ID. NO. 381,  
 SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ. ID. NO. 389, SEQ.  
 ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID. NO. 397, SEQ. ID.  
 NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO. 405, SEQ. ID. NO.  
 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413, SEQ. ID. NO. 415,  
 20 SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ.  
 ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID.  
 NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO.  
 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449,  
 SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ.  
 25 ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID.  
 NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO.  
 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483,  
 SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ.  
 ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO:  
 30 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and  
 SEQ ID NO: 511, wherein the fragment is at least 10, preferably 20, 30, 50, 70, 100,  
 or 150 amino acids in length.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a variant of said fragment, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

5 It is still another object of the invention to provide an isolated polypeptide comprising an amino acid sequence that is at least 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ.  
10 ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61,  
15 SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID.  
20 NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID.  
25 NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID.  
30 NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID.

NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID.  
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243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,  
5 SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.  
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10 ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.  
NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO.  
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SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.  
ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.  
15 NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO.  
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SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.  
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20 SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.  
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25 ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.  
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SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.  
ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID.  
30 NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.  
473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481,  
SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.  
ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:



499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated polypeptide comprising a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.

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 5 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285,  
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 311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319,  
 10 SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.  
 ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.  
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 15 ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO:  
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 ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID.  
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 20 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,  
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 ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.  
 NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO.  
 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447,  
 25 SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.  
 ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID.  
 NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.  
 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481,  
 SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.  
 30 ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:  
 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ  
 ID NO: 509 and SEQ ID NO: 511, wherein the fragment is at least 40, preferably 60,  
 80, 100, 150, 200, or 250 amino acids in length.

It is still a further object of the invention to provide an isolated polypeptide comprising a variant of said fragment, especially naturally occurring allelic variants, the expression of which may be significant in the manner by which different persons in the human population perceive odors differently, both on a qualitative and  
5 quantitative level, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

It is still another object of the invention to provide agonists, including inverse agonists, or antagonists of such ORs, or fragments or variants thereof.

It is yet another object of the invention to provide methods for representing the  
10 perception of odor and/or for predicting the perception of odor in a mammal, including in a human. Preferably, such methods may be performed by using the ORs, or fragments or variants thereof, and genes encoding such ORs, or fragments or variants thereof, disclosed herein.

It is yet another object of the invention to provide novel molecules or combinations of  
15 molecules which elicit a predetermined olfactory perception in a mammal. Such molecules or compositions can be generated by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules; comparing the value of olfactory perception  
20 in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a  
25 predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

It is still a further object of the invention to provide a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising:  
30 a step of contacting said one or more compounds with the disclosed ORs, fragments or variants thereof, preferably wherein the mammal is a human.

It is another object of the invention to provided a method for simulating a fragrance, comprising: for each of a plurality of ORs, or fragments of variants thereof

disclosed herein, preferably human ORs, ascertaining the extent to which the OR interacts with the fragrance; and combining a plurality of compounds, each having a previously ascertained interaction with one or more of the ORs, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an OR can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80% or 90% or all of the receptors that are substantially stimulated by the fragrance.

In yet another aspect of the invention, a method is provided wherein a plurality of standard compounds are tested against a plurality of ORs, or fragments or variants thereof, to ascertain the extent to which the ORs each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

It is a further object of the invention to provide a method for representing olfactory perception of a particular smell in a mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  ORs of said vertebrate, where  $n$  is greater than or equal to 4,  $n$  is greater than or equal to 12;  $n$  is greater than or equal to 24,  $n$  is greater than or equal to 48;  $n$  is greater than or equal to 72;  $n$  is greater than or equal to 96;  $n$  is greater than or equal to 120;  $n$  is greater than or equal to 144;  $n$  is greater than or equal to 168;  $n$  is greater than or equal to 192;  $n$  is greater than or equal to 216, or  $n$  is greater than or equal to 256; and generating from said values a quantitative representation of olfactory perception. The ORs may be an olfactory receptor disclosed herein, or fragments or variants thereof, the representation may constitute a point or a volume in  $n$ -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the

providing step may comprise contacting a plurality of recombinantly produced ORs, or fragments or variants thereof, with a test composition and quantitatively measuring the interaction of said composition with said receptors.

It is yet another object of the invention to provide a method for predicting the  
5 olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  ORs of said vertebrate, where  $n$  is greater than or equal to 4  $n$  is greater than or equal to 12;  $n$  is greater than or equal to 24,  $n$  is greater than or equal to 48;  $n$  is  
10 greater than or equal to 72;  $n$  is greater than or equal to 96;  $n$  is greater than or equal to 120;  $n$  is greater than or equal to 144;  $n$  is greater than or equal to 168;  $n$  is greater than or equal to 192;  $n$  is greater than or equal to 216, or  $n$  is greater than or equal to 256; for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative  
15 representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  ORs of said vertebrate, where  $n$  is greater than or equal to 4,  $n$  is greater than or equal to 12;  $n$  is greater than or equal to 24,  $n$  is greater than or equal to 48;  $n$  is greater than or equal to 72;  $n$  is greater than or equal to 96;  $n$  is greater than or equal to 120;  $n$  is  
20 greater than or equal to 144;  $n$  is greater than or equal to 168;  $n$  is greater than or equal to 192;  $n$  is greater than or equal to 216, or  $n$  is greater than or equal to 273; for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of  
25 molecules yielding unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the  
30 one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known

olfactory perception in a mammal. The ORs used in this method may include an olfactory receptor, or fragment or variant thereof, disclosed herein.

#### Brief Description of the Drawings

5           Figure 1 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR1 through AOLFR52. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences  
10 AOLFR2 through AOLFR52 were analyzed for alignment with the AOLFR1 amino acid sequence.

          Figure 2 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins  
15 described herein are designated AOLFR54 through AOLFR109. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR55 through AOLFR109 were analyzed for alignment with the AOLFR54 amino acid sequence.

          Figure 3 illustrates the multiple sequence alignment derived for fifty novel  
20 ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR110 through AOLFR163. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR111 through AOLFR163 were analyzed for alignment with the  
25 AOLFR110 amino acid sequence.

          Figure 4 illustrates the multiple sequence alignment derived for fifty-four novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-four novel human olfactory receptors (hOR) proteins described herein are designated AOLFR165 through AOLFR217. The  
30 alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR166 through AOLFR217 were analyzed for alignment with the AOLFR165 amino acid sequence.

Figure 5 illustrates the multiple sequence alignment derived for fifty-two novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-two novel human olfactory receptors (hOR) proteins described herein, which are designated AOLFR218 through AOLFR328. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR219 through AOLFR328 were analyzed for alignment with the AOLFR218 amino acid sequence.

#### Detailed Description of the Invention

The invention thus provides isolated nucleic acid molecules encoding olfactory-cell-specific G protein-coupled receptors ("GPCRs"), and the polypeptides they encode. These nucleic acid molecules and the polypeptides that they encode are members of the olfactory receptor family. Other members of the olfactory receptor family are disclosed in Krautwurst, *et al.*, *Cell*, 95:917-26 (1998), and WO 0035274, the contents of which are herein incorporated by reference in their entireties.

According to one aspect of the invention, genes encoding over two hundred fifty distinct, novel human olfactory (odorant) receptors (also herein referred to ORs) have been identified in genome sequence databases. All of these receptor genes have been initially detected by computer DNA sequence analysis of genomic clones (unfinished High Throughput Genomic Sequence database accession numbers AB045359, AP002532, AP002533, AL365440, AC073487, AL359636, AL359955, AP002535, AB045365, AL359218, AC002555, AB045361, AL359512, AC023255, AL358773, AL357767, AL358874, AC068380, AC025283, AP002407, AC018700, AC022289, AC006313, AC002556, AC011571, AL121944, AC007194, AP001112, AC021660, AP000723, AC016856, AC018700, AP000818, AC00596, AP000916, AC011517, AP001112, AP000916, AC021427, AC021427, AC020884, AC019108, AL135841, AL133410, AF186996, AL138834, AC009237, AC025249, AC010930, AC009758, AC009642, AC009758, AC025249, AF101706, AC009642, AC025249, AC021660, AC011647, AC011711, AC09642, AC020597, AC011711, AC019088, AC022882, AC011571, AL121944, AP000435, AC012616, AC010332, AC010766, AP000743, AC021809, AC011879, AC021304, AC023226, AL160314, AC021304, AC020380, AC011904, AC004977, AC021304, AP000868, AP000825, AC023080, AC022207, AC121986, AC010814, AC018700, AC021304, AC008620, AC011537,

AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, AP001803, AP001804, AL353767, AP001884, AC026083, 5 AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, AP002826, AL359636, AL391534, AC055731, AC076959, 10 AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes.

Alternatively, nucleic acids encoding the olfactory receptors (ORs) and polypeptides of the invention can be isolated from a variety of sources, genetically 15 engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 0035374, which is herein incorporated by reference in its entirety.

These nucleic acids provide valuable probes for the identification of olfactory cells, as the nucleic acids are specifically expressed in olfactory cells. They can also 20 serve as tools for the generation of sensory topographical maps that elucidate the relationship between olfactory cells and olfactory sensory neurons leading to olfactory centers in the brain. Furthermore, the nucleic acids and the polypeptides they encode can be used as probes to elucidate olfactory-induced behaviors.

The invention also provides methods of screening for modulators, *e.g.*, 25 activators, inhibitors, stimulators, enhancers, agonists, inverse agonists and antagonists, of the ORs, or fragments or variants thereof, of the invention. Such modulators of olfactory transduction are useful for pharmacological and genetic modulation of olfactory signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of olfactory cell activity. These 30 modulator compounds can then be used in the food, pharmaceutical, and cosmetic industries to customize odors and fragrances.

Thus, the invention provides assays for olfactory modulation, where the ORs, or fragments or variants thereof, of the invention act as direct or indirect reporter



molecules for the effect of modulators on olfactory transduction. The ORs, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo* and *ex vivo*. In one embodiment, the ORs, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g.*, Mistili *et al.*, *Nature Biotech.*, 15:961-64 (1997)). In another embodiment, the ORs, or fragments or variants thereof, can be expressed in host cells, and modulation of olfactory transduction via OR activity can be assayed by measuring changes in  $\text{Ca}^{2+}$  levels.

Methods of assaying for modulators of olfactory transduction include *in vitro* ligand binding assays using the ORs of the invention, or fragments or variants thereof. More particularly, such assays can use the ORs; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular  $\text{Ca}^{2+}$  levels; and neurotransmitter release.

The invention also provides for methods of detecting olfactory nucleic acid and protein expression, allowing for the investigation of olfactory transduction regulation and specific identification of olfactory receptor cells. The ORs, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying olfactory receptor cells. Olfactory receptor cells can be identified using techniques such as reverse transcription and amplification of mRNA, isolation of total RNA or poly A<sup>+</sup> RNA, northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, western blots, and the like.

#### **A. Identification and Characterization of Olfactory Receptors**

The amino acid sequences of the ORs and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various

amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of: from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *PNAS*, 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1997) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued

threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990)). These initial neighborhood word hits act as seeds for initiating  
5 searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a  
10 scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and  
15 X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *PNAS*, 89:10915 (1989))  
20 alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-  
25 called "tree" or "dendogram" showing the clustering relationships used to create the alignment (*see, e.g.*, Figure 2). PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351-60 (1987). The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of  
30 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple

extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using  
5 PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, *e.g.*, version 7. 0 (Devereaux *et al.*, *Nuc. Acids Res.* 12:387-395 (1984) encoded by the genes were  
10 derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian olfactory receptor family, each of the odorant receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most  
15 preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative OR proteins generally having lengths of approximately 290 to approximately 400 amino acid residues that contain seven transmembrane domains, as  
20 predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor 7-transmembrane (7TM) superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the ORs identified herein has a characteristic sequence signature of an olfactory receptor. In particular, all the identified sequences contain very close  
25 matches to the following consensus amino acid motifs (Mombaerts, 1999, Pilpel 1999): EFILL (SEQ ID NO: 513) before transmembrane domain 1, LHTPMY (SEQ ID No: 514) in intracellular loop 1, MAYDRYVAIC (SEQ ID NO: 510) at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5, FSTCSSH (SEQ ID NO: 516) in the beginning of  
30 transmembrane domain 6, and PMLNPF (SEQ ID NO: 517) in transmembrane domain 7. Combination of all the above-mentioned structural features of the identified genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

As noted above, complete or partial sequences of numerous human and other eukaryotic olfactory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human olfactory receptors, which suggests their different specificity in odorant recognition. Therefore, these novel receptors and their genes can be used, alone or in combination with known olfactory receptors, in developing detection systems and assays for chemically distinct types of odorants not recognized by the known receptors, as well as for diagnostic and research purposes.

**B. Definitions**

As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

“OR” refers to one or more members of a family of G protein-coupled receptors that are expressed in olfactory cells. Olfactory receptor cells can also be identified on the basis of morphology (*see, e.g., Roper, supra*), or by the expression of proteins specifically expressed in olfactory cells. OR family members may have the ability to act as receptors for olfactory transduction.

“OR” nucleic acids encode a family of GPCRs with seven transmembrane regions that have “G protein-coupled receptor activity,” *e.g.,* they may bind to G proteins in response to extracellular stimuli and promote production of second messengers such as IP<sub>3</sub>, cAMP, cGMP, and Ca<sup>2+</sup> via stimulation of enzymes such as phospholipase C and adenylate cyclase (for a description of the structure and function of GPCRs, *see, e.g., Fong, supra*, and Baldwin, *supra*). A single olfactory cell may contain many distinct OR polypeptides.

Topologically, certain chemosensory GPCRs have an “N-terminal domain;” “extracellular domains;” “transmembrane domains” comprising seven transmembrane regions, and corresponding cytoplasmic, and extracellular loops; “cytoplasmic domains,” and a “C-terminal domain” (*see, e.g., Hoon et al., Cell*, 96:541-51 (1999); Buck & Axel, *Cell*, 65:175-87 (1991)). These domains can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs that identify hydrophobic and hydrophilic domains (*see, e.g., Stryer, Biochemistry*, (3rd ed. 1988); *see also* any of a number of Internet based sequence analysis programs, such as those found at dot.imngen.bcm.tmc.edu). Such domains are useful

for making chimeric proteins and for in vitro assays of the invention, *e.g.*, ligand binding assays.

“Extracellular domains” therefore refers to the domains of OR polypeptides that protrude from the cellular membrane and are exposed to the extracellular face of the cell. Such domains generally include the “N terminal domain” that is exposed to the extracellular face of the cell, and optionally can include portions of the extracellular loops of the transmembrane domain that are exposed to the extracellular face of the cell, *i.e.*, the loops between transmembrane regions 2 and 3, between transmembrane regions 4 and 5, and between transmembrane regions 6 and 7.

The “N terminal domain” region starts at the N-terminus and extends to a region close to the start of the transmembrane domain. “Transmembrane domain,” which comprises the seven “transmembrane regions,” refers to the domain of OR polypeptides that lies within the plasma membrane, and may also include the corresponding cytoplasmic (intracellular) and extracellular loops. The seven transmembrane regions and extracellular and cytoplasmic loops can be identified using standard methods, as described in Kyte & Doolittle, *J. Mol. Biol.*, 157:105-32 (1982)), or in Stryer, *supra*. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below. These transmembrane domains are useful for *in vitro* ligand-binding assays, both soluble and solid phase.

“Cytoplasmic domains” refers to the domains of OR polypeptides that face the inside of the cell, *e.g.*, the “C terminal domain” and the intracellular loops of the transmembrane domain, *e.g.*, the intracellular loop between transmembrane regions 1 and 2, the intracellular loop between transmembrane regions 3 and 4, and the intracellular loop between transmembrane regions 5 and 6. “C terminal domain” refers to the region that spans the end of the last transmembrane domain and the C-terminus of the protein, and which is normally located within the cytoplasm.

The term “ligand-binding region” or “ligand-binding domain” refers to sequences derived from a chemosensory receptor, particularly an olfactory receptor,

that substantially incorporates at least transmembrane domains II to VII. The ligand-binding region may be capable of binding a ligand, and more particularly, an odorant.

The phrase “functional effects” in the context of assays for testing compounds that modulate OR family member mediated olfactory transduction includes the determination of any parameter that is indirectly or directly under the influence of the receptor, *e.g.*, functional, physical and chemical effects. It includes ligand binding, changes in ion flux, membrane potential, current flow, transcription, G protein binding, GPCR phosphorylation or dephosphorylation, signal transduction, receptor-ligand interactions, second messenger concentrations (*e.g.*, cAMP, cGMP, IP3, or intracellular  $\text{Ca}^{2+}$ ), *in vitro*, *in vivo*, and *ex vivo* and also includes other physiologic effects such increases or decreases of neurotransmitter or hormone release.

By “determining the functional effect” in the context of assays is meant assays for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an OR family member, *e.g.*, functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index), hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties, patch clamping, voltage-sensitive dyes, whole cell currents, radioisotope efflux, inducible markers, oocyte OR gene expression; tissue culture cell OR expression; transcriptional activation of OR genes; ligand-binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP, cGMP, and inositol triphosphate (IP3); changes in intracellular calcium levels; neurotransmitter release, and the like.

“Inhibitors,” “activators,” and “modulators” of OR genes or proteins are used interchangeably to refer to inhibitory, activating, or modulating molecules identified using *in vitro* and *in vivo* assays for olfactory transduction, *e.g.*, ligands, agonists, antagonists, and their homologs and mimetics. Inhibitors are compounds that, *e.g.*, bind to, partially or totally block stimulation, decrease, prevent, delay activation, inactivate, desensitize, or down regulate olfactory transduction, *e.g.*, antagonists. Activators are compounds that, *e.g.*, bind to, stimulate, increase, open, activate, facilitate, enhance activation, sensitize, or up regulate olfactory transduction, *e.g.*, agonists. Modulators include compounds that, *e.g.*, alter the interaction of a receptor

with: extracellular proteins that bind activators or inhibitor (*e.g.*, ebnerin and other members of the hydrophobic carrier family); G proteins; kinases (*e.g.*, homologs of rhodopsin kinase and beta adrenergic receptor kinases that are involved in deactivation and desensitization of a receptor); and arrestins, which also deactivate and desensitize receptors. Modulators can include genetically modified versions of OR family members, *e.g.*, with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, small chemical molecules and the like. Such assays for inhibitors and activators include, *e.g.*, expressing OR family members in cells or cell membranes, applying putative modulator compounds, in the presence or absence of tastants, *e.g.*, sweet tastants, and then determining the functional effects on olfactory transduction, as described above. Samples or assays comprising OR family members that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of modulation. Control samples (untreated with modulators) are assigned a relative OR activity value of 100%. Inhibition of a OR is achieved when the OR activity value relative to the control is about 80%, optionally 50% or 25-0%. Activation of an OR is achieved when the OR activity value relative to the control is 110%, optionally 150%, optionally 200-500%, or 1000-3000% higher.

The terms "purified," "substantially purified," and "isolated" as used herein refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the



meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

5           As used herein, the term "isolated," when referring to a nucleic acid or polypeptide refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the body, including (1) the purification from other naturally-occurring associated structures or  
10       compounds, or (2) the association with structures or compounds to which it is not normally associated in the body are within the meaning of "isolated" as used herein. The nucleic acids or polypeptides described herein may be isolated or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processed known to those of skill in the  
15       art.

          As used herein, the terms "amplifying" and "amplification" refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.*, specific degenerate oligonucleotide  
20       primer pairs) for amplifying (*e.g.*, by polymerase chain reaction, PCR) naturally expressed (*e.g.*, genomic or mRNA) or recombinant (*e.g.*, cDNA) nucleic acids of the invention (*e.g.*, tastant-binding sequences of the invention) *in vivo* or *in vitro*.

          The term "7- transmembrane receptor" means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma  
25       membrane seven times (thus, the seven domains are called "transmembrane" or "TM" domains TM I to TM VII). The families of olfactory and certain taste receptors each belong to this super-family. 7-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

30           The term "library" means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated chemosensory, particularly olfactory receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of

vectors that incorporate the amplified ligand-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding an olfactory receptor.

The term “nucleic acid” or “nucleic acid sequence” refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded  
5 form. The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones (*see e.g., Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Antisense Strategies, Annals of the N.Y. Acad. of Sci.*, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan  
10 *J. Med. Chem.* 36:1923-1937 (1993); *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata, *Toxicol. Appl. Pharmacol.* 144:189-197 (1997); Strauss-Soukup, *Biochemistry* 36:8692-8698 (1997); Samstag, *Antisense Nucleic Acid Drug Dev*, 6:153-156 (1996)).

Unless otherwise indicated, a particular nucleic acid sequence also implicitly  
15 encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating, *e.g.*, sequences in which the third position of one or more selected codons is substituted with mixed-base and/or deoxyinosine residues (Batzner *et al.*, *Nucleic  
20 Acid Res.*, 19:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.*, 260:2605-08 (1985); Rossolini *et al.*, *Mol. Cell. Probes*, 8:91-98 (1994)). The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

The terms “polypeptide,” “peptide” and “protein” are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid  
25 polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

The term “plasma membrane translocation domain” or simply “translocation domain” means a polypeptide domain that, when incorporated into the amino terminus  
30 of a polypeptide coding sequence, can with great efficiency “chaperone” or “translocate” the hybrid (“fusion”) protein to the cell plasma membrane. For instance, a “translocation domain” may be derived from the amino terminus of the bovine rhodopsin receptor polypeptide. In one embodiment, the translocation domain may be

functionally equivalent to an exemplary translocation domain (5'-MNGTEGPNFYVPFSNKTGVV; SEQ ID NO: 518). However, rhodopsin from any mammal may be used, as can other translocation facilitating sequences. Thus, the translocation domain is particularly efficient in translocating 7-transmembrane fusion proteins to the plasma membrane, and a protein (*e.g.*, an olfactory receptor polypeptide) comprising an amino terminal translocating domain will be transported to the plasma membrane more efficiently than without the domain. However, if the N-terminal domain of the polypeptide is active in binding, the use of other translocation domains may be preferred.

“Functional equivalency” means the domain’s ability and efficiency in translocating newly translated proteins to the plasma membrane as efficiently as exemplary SEQ ID NO: 518 under similar conditions; relative efficiencies can be measured (in quantitative terms) and compared, as described herein. Domains falling within the scope of the invention can be determined by routine screening for their efficiency in translocating newly synthesized polypeptides to the plasma membrane in a cell (mammalian, *Xenopus*, and the like) with the same efficiency as the twenty amino acid long translocation domain SEQ ID NO: 518, as described in detail below.

The “translocation domain,” “ligand-binding domain”, and chimeric receptors compositions described herein also include “analogs,” or “conservative variants” and “mimetics” (“peptidomimetics”) with structures and activity that substantially correspond to the exemplary sequences. Thus, the terms “conservative variant” or “analog” or “mimetic” refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the polypeptide’s (the conservative variant’s) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, *etc.*) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity. Conservative substitution tables providing functionally similar amino acids are well known in the art.

More particularly, “conservatively modified variants” applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences,

conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids  
5 encode any given protein.

For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide.

10 Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only  
15 codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

Conservative substitution tables providing functionally similar amino acids are well known in the art. For example, one exemplary guideline to select conservative  
20 substitutions includes (original residue followed by exemplary substitution): ala/gly or ser; arg/lys; asn/gln or his; asp/glu; cys/ser; gln/asn; gly/asp; gly/ala or pro; his/asn or gln; ile/leu or val; leu/ile or val; lys/arg or gln or glu; met/leu or tyr or ile; phe/met or leu or tyr; ser/thr; thr/ser; trp/tyr; tyr/trp or phe; val/ile or leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that  
25 are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g.,* Creighton, *Proteins*, W.H. Freeman and Company (1984); Schultz and Schimer, *Principles of*  
30 *Protein Structure*, Springer-Verlag (1979)). One of skill in the art will appreciate that the above-identified substitutions are not the only possible conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In

addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

5 The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains, ligand-binding domains, or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or may be a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can  
10 also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity.

As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the  
15 invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues  
20 which induce secondary structural mimicry, *i.e.*, to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or  
25 coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH<sub>2</sub>- for -C(=O)-NH-), aminomethylene (CH<sub>2</sub>-NH), ethylene, olefin  
30 (CH=CH), ether (CH<sub>2</sub>-O), thioether (CH<sub>2</sub>-S), tetrazole (CN<sub>4</sub>), thiazole, retroamide, thioamide, or ester (*see, e.g.*, Spatola, *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, 7:267-357, "Peptide Backbone Modifications," Marcell Dekker, NY (1983)). A polypeptide can also be characterized as a mimetic by

containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include <sup>32</sup>P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are optionally directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one

source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

5 A "promoter" is defined as an array of nucleic acid sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter  
10 that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the  
15 expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (e.g., "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other  
20 biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, e.g., inducible or constitutive expression of a fusion protein comprising a translocation domain of the  
25 invention and a nucleic acid sequence amplified using a primer of the invention.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

30 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acid, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer

sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology - Hybridisation with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent

5 conditions are selected to be about 5-10° C lower than the thermal melting point (T<sub>m</sub>) for the specific sequence at a defined ionic strength pH. The T<sub>m</sub> is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T<sub>m</sub>, 50% of the probes are occupied at

10 equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the

15 addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, optionally 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1 % SDS at 65°C. Such

20 hybridizations and wash steps can be carried out for, e.g., 1, 2, 5, 10, 15, 30, 60; or more minutes.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially related if the polypeptides that they encode are substantially related. This occurs, for example, when a copy of a nucleic acid is created using the maximum

25 codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1x SSC at 45°C. Such hybridizations and wash steps can be carried out for, e.g., 1, 2, 5, 10, 15, 30, 60, or

30 more minutes. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.



“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one “light” (about 25 kDa) and one “heavy” chain (about 50-70 kDa). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chains respectively.

A “chimeric antibody” is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, *etc.*; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

An “anti-OR” antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a OR gene, cDNA, or a subsequence thereof.

The term “immunoassay” is an assay that uses an antibody to specifically bind an antigen. The immunoassay is characterized by the use of specific binding properties of a particular antibody to isolate, target, and/or quantify the antigen.

The phrase “specifically (or selectively) binds” to an antibody or, “specifically (or selectively) immunoreactive with,” when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and do not substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular

protein. For example, polyclonal antibodies raised to an OR family member from specific species such as rat, mouse, or human can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the OR polypeptide or an immunogenic portion thereof and not with other proteins, except for orthologs or polymorphic variants and alleles of the OR polypeptide. This selection may be achieved by subtracting out antibodies that cross-react with OR molecules from other species or other OR molecules. Antibodies can also be selected that recognize only OR GPCR family members but not GPCRs from other families. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g., Harlow & Lane, Antibodies, A Laboratory Manual, (1988), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity*). Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

The phrase “selectively associates with” refers to the ability of a nucleic acid to “selectively hybridize” with another as defined above, or the ability of an antibody to “selectively (or specifically) bind to a protein, as defined above.

The term “expression vector” refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, i.e., drive only transient expression in a cell. The term includes recombinant expression “cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

By “host cell” is meant a cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, HEK-293, and the like, *e.g.,* cultured cells, explants, and cells *in vivo*.

### C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the ORs, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand-binding regions and libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (*e.g.*, promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, *e.g.*, bacterial, yeast, insect or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, *e.g.*, Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature.

See, e.g., Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes*, Part I, Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, e.g., analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, e.g., fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (e.g., SDS-PAGE), RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (PCR Protocols, a Guide to Methods and Applications, ed. Innis. Academic Press, N.Y. (1990) and PCR Strategies, ed. Innis, Academic Press, Inc., N.Y. (1995), ligase chain reaction (LCR) (see, e.g., Wu, *Genomics* 4:560 (1989); Landegren, *Science* 241:1077,(1988); Barringer, *Gene* 89:117 (1990)); transcription amplification (see, e.g., Kwoh, *PNAS*, 86:1173 (1989)); and, self-sustained sequence replication (see, e.g., Guatelli, *PNAS*, 87:1874 (1990)); Q Beta replicase amplification (see, e.g., Smith, *J. Clin. Microbiol.* 35:1477-1491 (1997)); automated Q-beta replicase amplification assay (see, e.g., Burg, *Mol. Cell. Probes* 10:257-271 (1996)) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307-316 (1987); Sambrook;

Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563-564 (1995).

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, *e.g.*, U.S. Pat. No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that, when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the ligand-binding region coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted ligand-binding domain comprises substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify ligand-binding regions of olfactory receptor proteins. These domain regions may vary for different ligands, and more particularly odorants; thus, what may be a minimal binding region for one ligand, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane OR.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL3' (SEQ ID NO: 519). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII).

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI 3' (SEQ ID NO: 520) (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3' (SEQ ID NO: 521)). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL (SEQ ID NO: 522), encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CANGT-3' (SEQ ID NO: 522). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) (SEQ ID NO: 523) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (*see, e.g., Rose, Nucleic Acids Res.* 26:1628-1635 (1998); Singh, *Biotechniques*, 24:318-19 (1998)).

Means to synthesize oligonucleotide primer pairs are well known in the art. "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g., Hoops, Nucleic Acids Res.* 25:4866-4871 (1997). Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g., Morales, Nat. Struct. Biol.* 5:950-954 (1998)). For example, two degenerate bases can be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g., Hill, PNAS*, 95:4258-63 (1998)). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine,3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, see above). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 524) and  
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 525).
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 526); and  
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 527)
- (c) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)GG-3' (SEQ ID NO: 528) and  
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 558)

Nucleic acids that encode ligand-binding regions of olfactory receptors may be generated by amplification (*e.g., PCR*) of appropriate nucleic acid sequences using

degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, e.g., olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (*see, e.g.,* Buiakova, *PNAS*, 93:9858-63 (1996)). Shirley, *Eur. J. Biochem.* 32:485-494 (1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211-216 (1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, e.g., antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260-8270 (1999), describes differentiated olfactory receptor-expressing cells in culture that respond to odorants, as measured by an influx of calcium.

In one embodiment, hybrid protein-coding sequences comprising nucleic acids ORs fused to the translocation sequences described herein may be constructed. Also provided are hybrid ORs comprising the translocation motifs and ligand-binding domains of olfactory receptors. These nucleic acid sequences can be operably linked to transcriptional or translational control elements, e.g., transcription and translation initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can also be used to express the fusion polypeptide receptor, including, e.g., a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and



distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227-236 (1998)). Receptor genes are normally expressed in a small subset of neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural  
5 sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

In another embodiment, fusion proteins, either having C-terminal or, more preferably, N-terminal translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional  
10 elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the  
15 FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g.*, Ottavi, *Biochimie* 80:289-293 (1998)), subtilisin protease recognition motif (*see, e.g.*, Polyak, *Protein Eng.* 10:615-619 (1997)); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane  
20 expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a polypeptide-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g.*, Williams, *Biochemistry* 34:1787-1797 (1995)), and an amino terminal translocation domain. The histidine residues facilitate  
25 detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature (*see, e.g.*, Kroll, *DNA Cell. Biol.* 12:441-53 (1993)).

30 Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent

literature (see, e.g., Roberts, *Nature* 328:731 (1987); Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10 (1995); Sambrook; Tijssen; Ausubel). Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from  
5 natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (e.g., episomal expression systems). Selection markers can be incorporated into expression cassettes and vectors to confer  
10 a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (e.g., chloramphenicol, kanamycin, G418, bleomycin, hygromycin) or herbicide resistance (e.g., chlorosulfuron or Basta) to permit selection of those cells  
15 transformed with the desired DNA sequences (see, e.g., Blondelet-Rouault, *Gene* 190:315-17 (1997); Aubrecht, *J. Pharmacol. Exp. Ther.*, 281:992-97 (1997)). Because selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

20 A chimeric nucleic acid sequence may encode a ligand-binding domain within any 7-transmembrane polypeptide. 7-transmembrane receptors belong to a superfamily of transmembrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-transmembrane receptor polypeptides have  
25 similar primary sequences and secondary and tertiary structures, structural domains (e.g., TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that  
30 characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969-977 (1999); Rost, *Protein Sci.* 4:521-533 (1995). Periodicity detection enhancement and alpha

helical periodicity index can be done as by, *e.g.*, Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.*, Peitsch, *Receptors Channels* 4:161-164 (1996); Cronet, *Protein Eng.* 6:59-64 (1993) (homology and "discover modeling"); <http://bioinfo.weizmann.ac.il/>.

5           The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, *e.g.*, TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (*e.g.*, PCR) from mRNA of or cDNA derived from, *e.g.*, olfactory receptor-expressing neurons or genomic DNA.

Libraries of olfactory receptor ligand-binding TM domain sequences can  
10 include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, *e.g.*, homology modeling, Fourier analysis and helical periodicity (*see, e.g.*, Pilpel  
15 *supra*), as described above. Using this information sequences flanking the seven domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of,  
20 for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the olfactory receptors described herein, coupled to additional amino acids representing all or part of another  
25 G protein receptor, preferably a member of the 7TM superfamily. These chimeras can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the seven transmembrane protein described herein, and the  
30 remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled

in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous GPCR extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, *e.g.*, green fluorescent protein,  $\beta$ -gal, glutamate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to an olfactory receptor disclosed herein can be isolated using the nucleic acid probes described above. It is hypothesized that allelic differences in receptors may explain why there is a difference in olfactory sensation in different human subjects. Accordingly, the identification of such alleles may be significant, especially with respect to producing receptor libraries that adequately represent the olfactory capability of the human population, *i.e.*, which take into account allelic differences in different individuals. Alternatively, expression libraries can be used to clone olfactory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against an olfactory polypeptide, which also recognize and selectively bind to the olfactory receptor homolog.

Also within the scope of the invention are host cells for expressing the ORs, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the olfactory receptors, fragments, or variants of the invention, one of skill typically subclones the nucleic acid sequence of interest into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable

bacterial promoters are well known in the art and described, *e.g.*, in Sambrook *et al.* However, bacterial or eukaryotic expression systems can be used.

Any of the well-known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Sambrook *et al.*) It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.*, WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

#### **D. Immunological Detection of OR Polypeptides**

In addition to the detection of OR genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect ORs, *e.g.*, to identify olfactory receptor cells, and variants of OR family members. Immunoassays can be used to qualitatively or quantitatively analyze the ORs. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

##### **1. Antibodies to OR family members**

Methods of producing polyclonal and monoclonal antibodies that react specifically with a OR family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *supra*; Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature*, 256:495-97 (1975)). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by

immunizing rabbits or mice (*see, e.g., Huse et al., Science, 246:1275-81 (1989); Ward et al., Nature, 341:544-46 (1989)*).

A number of OR-comprising immunogens may be used to produce antibodies specifically reactive with a OR family member. For example, a recombinant OR protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the conserved motifs that are used to identify members of the OR family. Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used as an immunogen. Naturally occurring protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in the art. For example, an inbred strain of mice (*e.g.*, BALB/C mice) or rabbits may be immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard immunization protocol. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the OR. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (*see Harlow & Lane, supra*).

Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen may be immortalized, commonly by fusion with a myeloma cell (*see Kohler & Milstein, Eur. J. Immunol., 6:511-19 (1976)*). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a

vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275-1281 (1989).

5            Monoclonal antibodies and polyclonal sera are collected and titered against the immunogen protein in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Typically, polyclonal antisera with a titer of 109 or greater are selected and tested for their cross reactivity against non-OR proteins, or even other OR family members or other related proteins from other  
10            organisms, using a competitive binding immunoassay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a  $K_d$  of at least about 0.1 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

             Once OR family member specific antibodies are available, individual OR  
15            proteins can be detected by a variety of immunoassay methods. For a review of immunological and immunoassay procedures, *see Basic and Clinical Immunology* (Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*.

## 20            2.        Immunological binding assays

             OR proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (*see, e.g.*, U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, *see also Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993);  
25            *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case an OR family member or an antigenic subsequence thereof). The antibody (*e.g.*, anti-OR) may be produced by any of a number of means well known to those of skill in the art and as described above.

30            Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent may be a labeled OR polypeptide or a labeled anti-OR antibody. Alternatively, the

labeling agent may be a third moiety, such a secondary antibody that specifically binds to the antibody/OR complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g., Kronval et al., J. Immunol.*, 111:1401-1406 (1973); *Akerstrom et al., J. Immunol.*, 135:2589-2542 (1985)). The labeling agent can be modified with a detectable moiety, such as biotin, to which another molecule can specifically bind, such as streptavidin. A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

**a. Non-competitive assay formats**

Immunoassays for detecting an OR protein in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of antigen is directly measured. In one preferred "sandwich" assay, for example, the anti-OR antibodies can be bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the OR protein present in the test sample. The OR protein is thus immobilized is then bound by a labeling agent, such as a second OR antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g., streptavidin*, to provide a detectable moiety.

**b. Competitive assay formats**

In competitive assays, the amount of OR protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) OR



protein displaced (competed away) from an anti-OR antibody by the unknown OR protein present in a sample. In one competitive assay, a known amount of OR protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the OR. The amount of exogenous OR protein bound to the antibody is inversely proportional to the concentration of OR protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of OR protein bound to the antibody may be determined either by measuring the amount of OR protein present in a OR/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of OR protein may be detected by providing a labeled OR molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known OR protein is immobilized on a solid substrate. A known amount of anti-OR antibody is added to the sample, and the sample is then contacted with the immobilized OR. The amount of anti-OR antibody bound to the known immobilized OR protein is inversely proportional to the amount of OR protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

### c. Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, OR proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the OR polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percent cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related

homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the OR family can be used in cross-reactivity determinations.

5 The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a OR family member, to the immunogen protein (*i.e.*, OR protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding  
10 of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to specifically bind to the polyclonal antibodies generated to a OR immunogen.

15 Antibodies raised against OR conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the OR family, but not to GPCRs from other families.

Polyclonal antibodies that specifically bind to a particular member of the OR family, *e.g.*, AOLFR1, can be make by subtracting out cross-reactive antibodies using  
20 other OR family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human AOLFR1 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OR1 or mouse OR1.

#### **d. Other assay formats**

25 Western blot (immunoblot) analysis is used to detect and quantify the presence of OR protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that  
30 specifically bind the OR protein. The anti-OR polypeptide antibodies specifically bind to the OR polypeptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-OR antibodies.

Other, assay formats include liposome immunoassays (LIA), which use liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see Monroe et al., Amer. Clin. Prod. Rev.*, 5:34-41 (1986)).

5                   e.       **Reduction of non-specific binding**

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific  
10 binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

                  f.       **Labels**

15               The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such  
20 methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (*e.g.*, DYNABEADS<sup>TM</sup>) (SEQ ID NO: 529), fluorescent dyes (*e.g.*, fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (*e.g.*, <sup>3</sup>H, <sup>125</sup>I, <sup>35</sup>S, <sup>14</sup>C,  
25 or <sup>32</sup>P), enzymes (*e.g.*, horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (*e.g.*, polystyrene, polypropylene, latex, *etc.*).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety  
30 of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to another molecules (*e.g.*, streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a OR protein, or secondary antibodies that recognize anti-OR.

The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, *etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, *see* U.S. Patent No. 4,391,904.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

## **E. Detection of Olfactory Modulators**

Methods and compositions for determining whether a test compound specifically binds to a mammalian chemosensory, and more particularly, an olfactory receptor of the invention, both *in vitro* and *in vivo* are described below. Many aspects of cell physiology can be monitored to assess the effect of ligand-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical stimuli into electrical signals. An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. Some examples include the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The OR protein of the assay will typically be selected from a polypeptide having a sequence selected from SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID.

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NO. 403, SEQ. ID. NO. 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413, SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ. ID. NO. 495, SEQ. ID. NO. 497, SEQ. ID. NO. 499, SEQ. ID. NO. 501, SEQ. ID. NO. 503, SEQ. ID. NO. 505, SEQ. ID. NO. 507, SEQ. ID. NO. 509 and SEQ. ID. NO. 511, or conservatively modified variant thereof.

Alternatively, the OR protein of the assay can be derived from a eukaryote host cell and can include an amino acid subsequence having at least about 30-40% amino acid sequence identity to SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID.

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Preferably, the amino acid sequence identity will be at least 50-75% preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of an OR protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand-binding domain, subunit association domain, active site, and the like. Either the OR protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein. As discussed *infra*, the family of ORs provided herein exhibits substantial sequence similarity at both the DNA and protein level, but also significant dissimilarity. In particular, the members possess an average percentage sequence identity to other members of the family when determined over the full length of the gene by about 30%. Moreover, different members of the genes at the protein level exhibit an average on the order of about 40% sequence identity to other members of the family when the full length protein sequences are compared. However, while there exist differences, there are characteristic similarities, *e.g.* the consensus sequence already mentioned, which further define members of this novel genus of receptors.

Modulators of OR activity can be tested using OR polypeptides as described above, either recombinant or naturally occurring. The protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

## 1. In vitro binding assays

Olfactory transduction can also be examined *in vitro* with soluble or solid state reactions, using a full-length OR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a OR covalently linked to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of an OR. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises all or part of a OR polypeptide, as well an additional sequence that facilitates the localization of the OR to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein, *e.g.* bovine or another mammalian rhodopsin.

Ligand binding to a OR protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties.

Receptor-G protein interactions can also be examined. For example, binding of the G protein to the receptor or its release from the receptor can be examined. For example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins.

Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

In another embodiment of the invention, a GTP $\gamma$ S assay may be used. As described above, upon activation of a GPCR, the G $\alpha$  subunit of the G protein complex is stimulated to exchange bound GDP for GTP. Ligand-mediated stimulation of G protein exchange activity can be measured in a biochemical assay measuring the binding of added radioactively-labeled GTP $\gamma$ <sup>35</sup>S to the G protein in the presence of a putative ligand. Typically, membranes containing the chemosensory receptor of interest are mixed with a complex of G proteins. Potential inhibitors and/or activators and GTP $\gamma$ S are added to the assay, and binding of GTP $\gamma$ S to the G protein is measured. Binding can be measured by liquid scintillation counting or by any other means known in the art, including scintillation proximity assays (SPA). In other assays formats, fluorescently-labeled GTP $\gamma$ S can be utilized.

## **2. Fluorescence Polarization Assays**

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor odorant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the olfactory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nanoseconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the

polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the olfactory receptors of the invention, fluorescence-labeled odorants or auto-fluorescent odorants may be used.

Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

Where  $\parallel$  is the intensity of the emission light parallel to the excitation light plane and  $\perp$  is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For example, the Beacon <sup>®</sup> and Beacon 2000 <sup>™</sup> System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley, M. E. (1991) in Journal of Analytical Toxicology, pp. 236-240, which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity ( $\eta$ ), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$Rotational\ Relaxation\ Time = \frac{3\eta V}{RT}$$

The rotational relaxation time is small ( $\approx$  1 nanosecond) for small molecules (e.g. fluorescein) and large ( $\approx$  100 nanoseconds) for large molecules (e.g. immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been

used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

### 3. Solid state and soluble high throughput assays

5 In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc.; a domain that is covalently linked to a heterologous  
10 protein to create a chimeric molecule; an OR protein; or a cell or tissue expressing an OR protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based in vitro assays in a high throughput format, where the domain, chimeric molecule, OR protein, or cell or tissue expressing the OR is attached to a solid phase substrate.

15 In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate  
20 can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is also possible to assay multiple compounds in each plate well. Further, it is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More  
25 recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (*e.g.*, the olfactory  
30 transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural

binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals  
5 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody  
10 and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors,  
15 immunoglobulin receptors and antibodies, the cadherein family, the integrin family, the selectin family, and the like; *see, e.g.*, Pigott & Power, The Adhesion Molecule Facts Book I (1993)). Similarly, toxins and venoms, viral epitopes, hormones (*e.g.*, opiates, steroids, *etc.*), intracellular receptors (*e.g.*, which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D;  
20 peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes,  
25 polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about  
30 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethylene glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent that fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups that are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. See, e.g., Merrifield, *J. Am. Chem. Soc.*, 85:2149-54 (1963) (describing solid phase synthesis of, e.g., peptides); Geysen *et al.*, *J. Immun. Meth.*, 102:259-74 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron*, 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al.*, *Science*, 251:767-77 (1991); Sheldon *et al.*, *Clinical Chemistry*, 39(4):718-19 (1993); and Kozal *et al.*, *Nature Medicine*, 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

#### 4. Computer-based assays

Yet another assay for compounds that modulate OR protein activity involves computer assisted compound design, in which a computer system is used to generate a three-dimensional structure of an OR protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, e.g., ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a OR polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID  
NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID  
NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID  
NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID  
5 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID  
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID  
NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID  
NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID  
NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,  
10 SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID  
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,  
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NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,  
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15 NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,  
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NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,  
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID  
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,  
20 SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID  
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,  
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NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,  
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25 NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,  
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NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,  
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID  
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,  
30 SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID  
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,  
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SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID  
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5 SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID  
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,  
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID  
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,  
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID  
10 NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,  
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID  
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,  
SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID  
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,  
15 SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID  
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,  
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID  
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,  
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID  
20 NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,  
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, and  
conservatively modified versions thereof.

The amino acid sequence represents the primary sequence or subsequence of  
the protein, which encodes the structural information of the protein. At least 10  
25 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino  
acids) are entered into the computer system from computer keyboards, computer  
readable substrates that include, but are not limited to, electronic storage media (*e.g.*,  
magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM),  
information distributed by internet sites, and by RAM. The three-dimensional  
30 structural model of the protein is then generated by the interaction of the amino acid  
sequence and the computer system, using software known to those of skill in the art. .

The amino acid sequence represents a primary structure that encodes the  
information necessary to form the secondary, tertiary and quaternary structure of the

protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent accessible surfaces, and hydrogen bonding. Secondary energy terms include van der  
5 Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

The tertiary structure of the protein encoded by the secondary structure is then  
10 formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the  
15 computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand-binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of  
20 compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the OR protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

25 Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of OR genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used  
30 to identify patients having such mutated genes. Identification of the mutated OR genes involves receiving input of a first nucleic acid or amino acid sequence of a OR gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is

then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once the first and second sequences are compared, nucleotide or amino acid differences between the sequences are identified.

- 5 Such sequences can represent allelic differences in various OR genes, and mutations associated with disease states and genetic traits.

### 5. Cell-based binding assays

- In a preferred embodiment, an OR polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates its maturation and targeting through the secretory pathway. In a preferred embodiment, the heterologous sequence is a rhodopsin sequence, such as an N-terminal fragment of a rhodopsin. Such chimeric OR receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a functional G protein, *e.g.*, G $\alpha$ 15, that is capable of coupling the chimeric receptor to an intracellular signaling pathway or to a signaling protein such as phospholipase C. Activation of such chimeric receptors in such cells can be detected using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell.

- Activated GPCR receptors become substrates for kinases that phosphorylate the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of  $^{32}\text{P}$  from gamma-labeled GTP to the receptor, which can be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of G proteins. The kinase/arrestin pathway plays a key role in the desensitization of many GPCR receptors. For example, compounds that modulate the duration an olfactory receptor stays active would be useful as a means of prolonging a desired odor or cutting off an unpleasant one. For a general review of GPCR signal transduction and methods of assaying signal transduction, *see, e.g., Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al.*, *Nature*, 10:349:117-27 (1991); Bourne *et al.*, *Nature*, 348:125-32 (1990); Pitcher *et al.*, *Annu. Rev. Biochem.*, 67:653-92 (1998).

OR modulation may be assayed by comparing the response of an OR polypeptide treated with a putative OR modulator to the response of an untreated

control sample. Such putative OR modulators can include odorants that either inhibit or activate OR polypeptide activity. In one embodiment, control samples (untreated with activators or inhibitors) are assigned a relative OR activity value of 100. Inhibition of an OR polypeptide is achieved when the OR activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of an OR polypeptide is achieved when the OR activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electrical potential) of the cell or membrane expressing a OR protein. One means to determine changes in cellular polarization is by measuring changes in current (thereby measuring changes in polarization) with voltage-clamp and patch-clamp techniques, *e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575-1595 (1997)). Whole cell currents are conveniently determined using the standard. Other known assays include: radiolabeled ion flux assays and fluorescence assays using voltage-sensitive dyes (*see, e.g.*, Vestergaard-Bogind *et al.*, *J. Membrane Biol.*, 88:67-75 (1988); Gonzales & Tsien, *Chem. Biol.*, 4:269-277 (1997); Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185-193 (1991); Holevinsky *et al.*, *J. Membrane Biology*, 137:59-70 (1994)). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as  $\text{Ca}^{2+}$ , IP3, cGMP, or cAMP.

Preferred assays for GPCRs include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G protein coupled receptors as negative or positive controls to assess activity of tested compounds. In

assays for identifying modulatory compounds (*e.g.*, agonists, antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed in the Molecular Probes 1997 Catalog. For G protein coupled receptors, promiscuous G proteins such as G $\alpha$ 15 and G $\alpha$ 16 can be used in the assay of choice (Wilkie *et al.*, *PNAS*, 88:10049-53 (1991)). Such promiscuous G proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*, increases in second messengers such as IP<sub>3</sub>, which releases intracellular stores of calcium ions. Activation of some G protein coupled receptors stimulates the formation of inositol triphosphate (IP<sub>3</sub>) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature*, 312:315-21 (1984)). IP<sub>3</sub> in turn stimulates the release of intracellular calcium ion stores. Thus, a change in cytoplasmic calcium ion levels, or a change in second messenger levels such as IP<sub>3</sub> can be used to assess G protein coupled receptor function. Cells expressing such G protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (*see, e.g.*, Altenhofen *et al.*, *PNAS*, 88:9868-72 (1991) and Dhallan *et al.*, *Nature*, 347:184-187 (1990)). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*,

certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors, serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, OR protein activity is measured by expressing a  
5 OR gene in a heterologous cell with a promiscuous G protein that links the receptor to a phospholipase C signal transduction pathway (*see* Offermanns & Simon, *J. Biol. Chem.*, 270:15175-15180 (1995)). Optionally the cell line is HEK-293 (which does not naturally express OR genes) and the promiscuous G protein is G $\alpha$ 15/G $\alpha$ 16 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by  
10 measuring changes in intracellular Ca<sup>2+</sup> levels, which change in response to modulation of the OR signal transduction pathway via administration of a molecule that associates with a OR protein. Changes in Ca<sup>2+</sup> levels are optionally measured using fluorescent Ca<sup>2+</sup> indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be  
15 measured using immunoassays. The method described in Offermanns & Simon, *J. Bio. Chem.*, 270:15175-15180 (1995), may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159-164 (1994), may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent 4,115,538, herein  
20 incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and  
25 extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the  
30 presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing an OR protein of interest is contacted with a test compound for a sufficient time to effect any

interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent 5,436,128, herein incorporated by reference. The reporter genes can be, e.g., chloramphenicol acetyltransferase, luciferase, '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (*see, e.g.,* Mistili & Spector, *Nature Biotechnology*, 15:961-64 (1997)).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the OR protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the OR protein of interest.

#### **6. Transgenic non-human animals expressing olfactory receptors**

Non-human animals expressing one or more olfactory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand-binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of the translocation domains of the invention in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize odorants/ligands that can bind to a specific or sets of receptors. Such

vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

Means to infect/express the nucleic acids and vectors, either individually or as  
5 libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses. When electrodes are located on the olfactory bulb surface it is possible to record stable  
10 responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287-291 (1997)). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of one turbinate bone or were placed in corresponding positions on four turbinate  
15 bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950-1962 (1997); Scott, *J. Neurophysiol.* 75:2036-2049 (1996); Ezeh, *J. Neurophysiol.* 73:2207-2220 (1995). In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and medial surface of the turbinates (*see, e.g.*, Youngentob, *J.*  
20 *Neurophysiol.* 73:387-398 (1995)). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1-5 (1991)).

The OR sequences of the invention can be for example expressed in animal  
25 nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *PNAS*, 96:4040-45 (1999).

The endogenous olfactory receptor genes can remain functional and wild-type  
30 (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic



animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, "gene trap insertion" can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97-106 (1997)). The insertion of the exogenous is typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. Gene targeting via homologous recombination in pluripotent embryonic stem cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see* Bijvoet, *Hum. Mol. Genet.* 7:53-62 (1998); Moreadith, *J. Mol. Med.* 75:208-216 (1997); Tojo, *Cytotechnology* 19:161-165 (1995); Mudgett, *Methods Mol. Biol.* 48:167-184 (1995); Longo, *Transgenic Res.* 6:321-328 (1997); U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO 93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries of the invention can also be used as reagents to produce "knockout" human cells and their progeny. Likewise, the nucleic acids of the invention can also be used as reagents to produce "knock-ins" in mice. The human or rat OR gene sequences can replace the orthologous ORs in the mouse genome. In this way, a mouse expressing a human or rat OR can be produced. This mouse can then be used to analyze the function of human or rat ORs, and to identify ligands for such ORs.

#### **F. Modulators**

The compounds tested as modulators of an OR family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of an OR gene.

Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to  
5 screen large chemical libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka  
10 Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

The OR modulating compounds can be used in any number of consumer products, including, but not limited to, perfumes, fragrance compositions, deorderants, air fresheners, foods, drugs, *etc.*, or ingredients thereof, to thereby modulate the odor of the product, composition, or ingredient in a desired manner. As  
15 one of skill in the art will recognize, OR modulating compounds can be used to enhance desirable odors, to block malodors, or a combination thereof.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such  
20 "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual odorant compositions.

25 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a  
30 given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.*, 37:487-93 (1991) and Houghton *et al.*, *Nature*, 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (*e.g.*, PCT Publication No. WO 91/19735), encoded peptides (*e.g.*, PCT Publication WO 93/20242), random bio-oligomers (*e.g.*, PCT Publication No. WO 92/00091), benzodiazepines (*e.g.*, U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *PNAS*, 90:6909-13 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.*, 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.*, 114:9217-18 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.*, 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science*, 261:1303 (1993)), peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.*, 59:658 (1994)), nucleic acid libraries (Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (U.S. Patent 5,539,083), antibody libraries (Vaughn *et al.*, *Nature Biotechnology*, 14(3):309-14 (1996) and PCT/US96/10287), carbohydrate libraries (Liang *et al.*, *Science*, 274:1520-22 (1996) and U.S. Patent 5,593,853), small organic molecule libraries (benzodiazepines, Baum, *C&EN*, Jan 18, page 33 (1993); thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pynrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS (Advanced Chem Tech, Louisville KY), Symphony (Rainin, Woburn, MA), 433A (Applied Biosystems, Foster City, CA), 9050 Plus (Millipore, Bedford, MA)). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, NJ; Tripos, Inc., St. Louis, MO; 3D Pharmaceuticals, Exton, PA; Martek Biosciences; Columbia, MD; *etc.*).

**G. Methods for Representing and Predicting the Perception of Odor**

The invention also preferably provides methods for representing the perception of odor (or taste) and/or for predicting the perception of odor (or taste) in a mammal, including in a human. Preferably, such methods may be performed by using the  
5 receptors and genes encoding said olfactory receptors disclosed herein.

Also contemplated as within the invention, is a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising: contacting said one or more compounds with the disclosed receptors, preferably wherein the mammal is a human. Also contemplated as within the invention is a  
10 method for representing olfactory perception of a particular smell in a mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  olfactory receptors of said vertebrate, where  $n$  is greater than or equal to 4; and generating from said values a quantitative representation of olfactory perception. The olfactory receptors may be an olfactory receptor disclosed herein, the  
15 representation may constitute a point or a volume in  $n$ -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced olfactory receptors with a test composition and quantitatively measuring the interaction of said composition with said receptors.

Also contemplated as within the invention, is a method for predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of  
20 each of  $n$  olfactory receptors of said vertebrate, where  $n$  is greater than or equal to 4, for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  olfactory receptors of  
25 said vertebrate, where  $n$  is greater than or equal to 4, for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding  
30

unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal. The olfactory receptors used in this method may include an olfactory receptor disclosed herein.

10 In another embodiment, novel molecules or combinations of molecules are generated which elicit a predetermined olfactory perception in a mammal by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules as described above; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules as described above; comparing the value of olfactory perception in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

25 In another embodiment of the invention, there is provided a method for simulating a fragrance, comprising: for each of a plurality of cloned olfactory receptors, preferably human receptors, ascertaining the extent to which the receptor interacts with the fragrance; and combining a plurality of compounds, each having a previously-ascertained interaction with one or more of the receptors, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an olfactory receptor can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds

substantially stimulate at least 75%, 80% or 90% of the receptors that are substantially stimulated by the fragrance.

In another preferred embodiment of the invention, a plurality of standard compounds are tested against a plurality of olfactory receptors to ascertain the extent to which the receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

#### H. Kits

OR genes and their homologs are useful tools for identifying olfactory receptor cells, for forensics and paternity determinations, and for examining olfactory transduction. OR family member-specific reagents that specifically hybridize to OR nucleic acids, such as AOLFR1 probes and primers, and OR family member-specific reagents that specifically bind to an OR protein, *e.g.*, OR antibodies are used to examine olfactory cell expression and olfactory transduction regulation.

Nucleic acid assays for the presence of DNA and RNA for an OR family member in a sample include numerous techniques are known to those skilled in the art, such as southern analysis, northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such a form so as to be available for hybridization within the cell, while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*, *Biotechniques*, 4:230-50 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, an OR protein can be detected with the various immunoassay

techniques described above. The test sample is typically compared to both a positive control (e.g., a sample expressing a recombinant OR protein) and a negative control.

The present invention also provides for kits for screening for modulators of OR family members. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise any one or more of the following materials: OR nucleic acids or proteins, reaction tubes, and instructions for testing OR activity. Optionally, the kit contains a biologically active OR receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

### EXAMPLES

Genomic, predicted amino acid sequence, and predicted coding sequences (cds), of novel G protein-coupled human odorant receptors, and classes of such receptors, are described. Each example describes a discrete protein and nucleic acid pair. Accordingly, Example 1 describes SEQ. ID. NOS. 1 and 2, for the human olfactory receptor protein designated AOLFR1, and the human DNA encoding AOLFR1, respectively; Example 2 describes SEQ. ID. NOS. 3 and 4, for the human olfactory receptor protein designated AOLFR2, and the human DNA encoding AOLFR2, respectively; and so on in the manner described, through the final Example sequence.

In the protein sequences presented herein, the one-letter code X or Xaa refers to any of the twenty common amino acid residues. In the DNA sequences presented herein, the one letter codes N or n refers to any of the of the four common nucleotide bases, A, T, C, or G.

### EXAMPLES

#### **AOLFR1 sequences:**

MKTFSSFLQIGRNMHQGNQTTITEFILLGFFKQDEHQNLLFVLFLGMYLVTVIGNGLIIV AISLD  
TYLHTP MYLFLANLSFADISSISNSVPKMLVNIQTKSQSISYESCITQMYFSIVFVIDNLLGTM  
AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIALHTLLLIQLLFCNHNTLPHFFCDLAPLL  
KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCIIRAVLRVSSTQGWKAFSTCGSHLTVVLLFY  
GTIVGVYFFPSSTHPEDTDKIGAVLFTVVTMPINPFIYSLRNKDMKGALRKLINRKISSL (SEQ ID  
NO: 1)

ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA  
CCATCACTGAATTCATTCTCCTGGGATTTTCAAGCAGGATGAGCATCAAAACCTCCTCTTT  
GTGCTTTTCTTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATCATTGTGGCTA  
TCAGCTTGGATACGTACCTTCATACCCCATGTATCTCTCCTTGCCAATCTATCCTTTGCT  
GATATTCTCTCCATTTCCTCAACTCAGTCCCCAAAATGCTGGTGAATATTCAAACCAAGAGTC

AATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTTCTATTGTGTTTGTGCGTCATT  
 GACAAATTTGCTCTTGGGGACCATGGCCTATGACCACTTTGTGGCGATCTGCCACCCTCTGA  
 ATTATACAATTCTCATGCGGCCAGGTTTCGGCATTGCTCACAGTCATCTCATGGTTCTCT  
 AGTAATATTATTGCTCTGACACACACCCTTCTGCTCATTC AATTGCTCTTCTGTAACCACAA  
 5 CACTCTCCACACTTCTTCTGTGACTTGGCCCCCTCTGCTCAAACCTGTCTGTTTCTGATACAT  
 TGATCAATGAGCTTGTGTTGTTTATTGTGGGTTTATCAGTTATCATCTTCCCCTTTTACACTC  
 AGCTTCTTTTCTATGTCTGCATCATCAGAGCTGTCTGAGAGTATCTTCCACACAGGGAA  
 AGTGGAAGCCTTCTCCACTTGTGGCTCTCACCTGACAGTTGTATTACTGTTCTACGGAAC  
 CATTGTAGGCGTGTACTTTTCCCCTCTCCACTCACCTGAGGACACTGATAAGATTGGT  
 10 GCTGTCTATTCACTGTGGTGACCCCATGATAAACCCCTTCATCTACAGCTTGAGGAATA  
 AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTTCTTCCCTTTGA (SEQ  
 ID NO: 2)

**AOLFR2 sequences:**

15 MMMVLRNLSMEPTFALLGFTDYPKLQIPLFLVFLLMYVITVVGNLGMIIKINPKFHTPMYFFL  
 SHLSFVDFCYSSIVTPKLENLVMADKSIFYFSCMMQYFLSCTAVVTESFLLAVMAYDRFVAIC  
 NPLLYTVAMSQRLLCALLVAGSYLWGMFGLVLLCYALRLNFSGPNVINHFFCEYALISVSGS  
 DILPHLLLSFATFNEMCTLLIILTSYVFIVTVLKIRSVSGRHKAFSTWASHLTAITIFHGTILFL  
 YCVPNSKNSRQTVKVASVFYTVVNPMLNPPIYSLRNKDVKDAFWKLIHTQVPFH (SEQ ID NO:  
 20 3)

ATGATGATGGTTTTAAGGAATCTGAGCATGGAGCCCACCTTTGCCCTTTTAGGTTTCACAG  
 ATTACCCAAAGCTTCAGATTCCTCTCTTCTTGTGTTTCTGCTCATGTATGTTATCACAGTG  
 GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAACCCCAAATTTCACTCTCTATGT  
 25 ACTTTTTCTTAGTCACCTCTCTTTTGTGATTTTGTGTTACTCTTCCATTGTCACTCCCAAGC  
 TGCTTGAGAACTTGGTAATGGCAGATAAAAGCATCTTCTACTTTAGCTGCATGATGCAGTA  
 CTTCTGTCTGCACTGCTGTGGTGACAGAGTCTTCTTGTGCTGGCAGTGATGGCCTATGAC  
 CGCTTTGTGGCCATCTGCAATCCTCTGCTTTATACAGTGGCCATGTCACAGAGGCTCTGTG  
 CCCTGCTGGTGGCTGGGTCATATCTCTGGGGCATGTTTGGCCCCCTGGTACTCCTTTGTTAT  
 30 GCTCTCCGGTTAAACTTCTCTGGACCTAATGTAATCAACCACTTCTTTTGTGAGTATACTGC  
 TCTCATCTCTGTGCTGGCTCTGATATACTCATCCCCACCTGCTGCTTTTCTAGCTTCGCCA  
 CTTTCAATGAGATGTGTACACTACTGATCATCTCACTTCTCTATGTTTTCTATTTTGTGACT  
 GTACTAAAAATCCGTTCTGTAGTGGGCGCCACAAAGCCTTCTCCACCTGGGCTCCCAAC  
 TGACTGCTATCACCATCTTCCATGGGACCATCTTTCTTCTTACTGTGTACCCCACTCCAAA  
 35 AACTCTCGGCAAAACAGTCAAAGTGGCTCTGTATTTTACACAGTTGTCAACCCCATGCTGA  
 ACCCTCCGATCTACAGCCTAAGGAATAAAGACGTGAAGGATGCTTTCTGGAAGTTAATACA  
 TACACAAGTTCCATTTTACTGA (SEQ ID NO: 4)

**AOLFR3 sequences:**

40 MLLTDRNTSGTTFLLGFSDYPELQVPLFLVFLAIYNVTVLGNIGLIVIIKINPKLHTPMYFFLSQ  
 LSFVDFCYSSIIAPKMLVNLVVKDRITISFLGCVVQFFFFCTFVVTESFLLAVMAYDRFVAICNPL  
 LYTVDMSQLCVLLVVGSYAWGVSCSLELTCSALKLCFHGFNTINHFFCEFSLLSLSCSDTYI  
 NQWLLFFLATFNEISTLLIVLTSYAFIVVTILKMRSVSGRRKAFSTCASHLTAITIFHGTILFLYCV  
 PNSKNSRHTVKVASVFYTVVIPMLNPLIYSLRNKDVKDTVTEILDTKVFSY (SEQ ID NO: 5)

45 ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTACCCCTCTTGGGCTTCTCAGATT  
 ACCCAGAAGTGAAGTCCCACTCTTCTGGTTTTTCTGGCCATCTACAATGTCACTGTGCTA  
 GGGAATATTGGGTTGATTGTGATCATCAAAATCAACCCCAAACCTGCATACCCCATGTACT  
 TTTTCTCTCAGCCAACCTCTCTTTGTGGATTCTGCTATTCTCCATCATTGCTCCCAAGATG  
 50 TTGGTGAACCTTGTGTCAAAGACAGAACCATTTCATTTTTAGGATGCGTAGTACAATTCT  
 TTTTCTTCTGTACCTTTGTGGTCACTGAATCCTTTTATTAGCTGTGATGGCCTATGACCGC  
 TTCGTGGCCATTTGCAACCTCTGCTCTACACAGTTGACATGTCCAGAACTCTGCGTGC  
 TGCTGGTTGTGGGATCCTATGCCTGGGGAGTCTCATGTTTCTTGGAACTGACGTGCTCTGC  
 TTTAAAGTTATGTTTTCATGGTTTCAACACAATCAATCACTTCTTCTGTGAGTTCTCCTCAC  
 55 TACTCTCCCTTTCTTGTCTGATACTTACATCAACCAGTGGCTGCTATTCTTTCTTGCCACC  
 TTTAATGAAATCAGCACACTACTCATCGTTCTCACATCTTATGCGTTTATTGTTGTAACCAT



5 CCTCAAGATGCGTTCAGTCAGTGGGCGCCGCAAAGCCTTCTCCACCTGTGCCTCCCACCTG  
 ACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTTTACTGTGTGCCAACTCCAAAAA  
 CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTACACCGTGGTGATCCCCATGTTGAAT  
 CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC  
 ACCAAAGTCTTCTCTTACTGA (SEQ ID NO: 6)

**AOLFR4 sequences:**

10 MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLS  
 LLDVMFSSVAPKVIVDTLSKSTTISLKGCLTQLFVEHFFGGVGIILLTVMAYDRYVAICKPLHY  
 TIIMSPRVCLMVGGAWVGGFMHAMIQLLFMYQIPFCGPNIIDHFICDLFQLLTLACTDTHILGL  
 LVTLNSGMMCVAFILILIASYTVILCSLKSYSKGRHKALSTCSSHLTVVVLFFVPCIFLYMRPV  
 VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

15 ATGGAAAATCAAAACAATGTGACTGAATTCATTCTTCTGGGTCTCACAGAGAACCTGGAGC  
 TGTGGAAAATATTTTCTGCTGTGTTTCTTGTGATGTATGTAGCCACAGTGTGGAAAATCT  
 ACTTATTGTGGTAACTATTATCACAAGTCAGAGTCTGAGGTACCTATGTATTTTTTCTTA  
 CCTTCTTGTCCCTTTTGGATGTCATGTTCTCATCTGTCGTTGCCCCAAGGTGATTGTAGAC  
 ACCCTCTCCAAGAGCACTACCATCTCTCTCAAAGGCTGCCTCACCCAGCTGTTTGTGGAGC  
 ATTTCTTTGGTGGTGTGGGGATCATCCTCCTCACTGTGATGGCCTATGACCGCTACGTGGC  
 20 CATCTGTAAGCCCCTGCACTACACGATCATCATGAGTCCACGGGTGTGCTGCCTAATGGTA  
 GGAGGGGCTTGGGTGGGGGGATTATGCACGCAATGATACAACTTCTCTTCATGTATCAAA  
 TACCCTTCTGTGGTCCTAATATCATAGATCACTTTATATGTGATTGTGTTTTCAGTTGTTGACA  
 CTTGCCTGCACGGACACCCACATCCTGGGCCTCTTAGTTACCCTCAACAGTGGGATGATGT  
 GTGTGGCCATCTTTCTTATCTTAATTGCGTCCTACACGGTCATCCTATGCTCCCTGAAGTCT  
 25 TACAGCTCTAAAGGGCGGCACAAAGCCCTCTCTACCTGCAGTCCCACCTCACGGTGGTTG  
 TATTGTTCTTTGTCCCTGTATTTTCTTGTACATGAGGCCTGTGGTCACTACCCCATAGAC  
 AAGGCAATGGCTGTGTCAGACTCAATCATCACCCCATGTTAAATCCCTTGATCTATACAC  
 TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAACTCTGGATGAAATGGGAGGCTTTGG  
 CTGGGAAATAA (SEQ ID NO: 8)

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**AOLFR5 sequences:**

35 MGKENCTTVAEFILLGLSDVPELRVCLFLLFLLIYGVTLNLANLGMIALIQVSSRLHTPMYFFLSH  
 LSSVDFCYSSIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLLAVMAYDRFVAICNPL  
 LYTVTMSWKVVRVELASCCYFCGTVCSLIHLCLALRIPFYRSNVINHHFFCDLPPVLSLACSDITVN  
 ETLLFLVATL NESVTIMILTSYLLILTTILKMGS AEGRHKAFSTCASHLTAITVFHGTVLSIYCRP  
 SSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKEALRKVMGSKIHS (SEQ ID NO: 9)

40 ATGGGCAAGGAAAACCTGCACCACTGTGGCTGAGTTCATTCTCCTTGGAATATCAGATGTCC  
 CTGAGTTGAGAGTCTGCCTCTTCTGCTGTTCTTCTCATCTATGGAGTCACGTTGTTAGCC  
 AACCTGGGCATGATTGCACTGATTACAGGTACAGTCTCGGCTCCACACCCCATGTACTTTT  
 TCCTCAGCCACTTGTCTCTGTAGATTTCTGCTACTCCTCAATAATTGTGCCAAAAATGTTG  
 GCTAATATCTTTAAACAAGGACAAAGCCATCTCCTCCTAGGGTGCATGGTGAATTCTACT  
 TGTTTTGCACTTGTGTGGTCACTGAGGTCTTCTGCTGGCCGTGATGGCCTATGACCGCTTT  
 GTGGCCATCTGTAACCCTTTGCTATACACAGTCACCATGTCTTGGAAGGTGCGTGTGGAGC  
 45 TGGCTTCTTGCTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCAATTTGTGCTTAGCTCTT  
 AGGATCCCCTTCTATAGATCTAATGTGATTAACCACTTTTTCTGTGATCTACCTCCTGTCTT  
 AAGTCTTGCTTGCTCTGATATCACTGTGAATGAGACACTGCTGTTCTGGTGGCCACTTTG  
 AATGAGAGTGTTACCATCATGATCATCCTCACCTCCTACCTGCTAATTCTCACCACCATCCT  
 GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCCACCTACA  
 50 GCTATCACTGTCTTCCATGGAACAGTCTTTCATTTATTGCAGGCCAGTTCAGGCAACA  
 GTGGAGATGCTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCTATGCTGAACTC  
 TGTGATCTACAGCCTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC  
 CAAAATTCACCTCTAG (SEQ ID NO: 10)

**AOLFR6 sequences:**

MMASERNQSSTPTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMYFFLS  
HLSLTDFCFSTVVTPKLLENLVVEYRTISFSGCIMQFCFACIFGVTETFMFLAAMAYDRFVAVCK  
5 PLLYTTIMSQKLCALLVAGSYTWGIVCSLILTYFLLDLSFCESTFINNFICDHSVIVSASYSDPYIS  
QRLCFIIAIFNEVSSLIILTSYMLIFTTIMKMRSASGRQKTFSTCASHLTAITIFHGTLFLYCVPNP  
KTSSLIVTVASVYFYTVAIPMLNPLIYSLRNKDINNMFEKLVVTKLIYH (SEQ ID NO: 11)

ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTTGGGTTTTTCAG  
AATACCCAGAAATCCAGGTTCCACTCTTTCTGGTTTTCTGTTCGTCTACACAGTCACTGTA  
10 GTGGGGAACCTTGGGCATGATAATAATCATCAGACTCAATTCAAACTCCATACAATCATGT  
ACTTTTTCTTAGTCACTTGTCTTGACAGACTTCTGTTTTTCCACTGTAGTTACACCTAAA  
CTGTTGGAGAACTTGGTTGTGGAATACAGAACCATCTCTTCTCTGGTTGCATCATGCAAT  
TTTGTGTTTGTCTGCATTTTGGAGTGACAGAACTTTCATGTTAGCAGCGATGGCTTATGAC  
CGTTTTGTGGCAGTTTGTAACCCCTTGCTGTATACCACTATTATGTCTCAGAAGCTCTGTGC  
15 TCTTCTGGTGGCTGGGTCCTATACATGGGGGATAGTGTGCTCCCTGATACTCACATATTTT  
CTTCTTGACTTATCGTTTTGTGAATCTACCTTCATAAATAATTTTATCTGTGACCACTCTGT  
AATTGTTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTATTATTGCCA  
TATTCAATGAGGTGAGCAGCCTAATTATCATTCTGACATCATATATGCTTATTTTCACTACC  
ATTATGAAGATGCGATCTGCAAGTGGGCGCCAGAAAACCTTCTCCACCTGTGCCTCCCACC  
20 TGACAGCCATCACTATCTCCATGGAATATCCTTTTCTTTACTGTGTTCTTAATCCTAAA  
ACTTCTAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGCTGA  
ACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTTGT  
CACCAAATTGATTACCACTGA (SEQ ID NO: 12)

**AOLFR7 sequences:**

MSYFYRLKLMKEAVLVKLPFTSLPLLQTLRKS RDMEIKNYSSSTSGFILLGLSSNPQLQKPLF  
AIFLIMYLLAAVGNVLIPAIYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFLSETKVISY  
VGCLAQMYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSISHLHSL  
FRVLLMSRLSFCASHIHKHFFCDTQPVKLKSCSDTSSSQMVMTETLAVIVTPFLCIHFSYLRIMV  
30 TVLRIPSAAGKWKAFTSCGSHLTAVALFYGSIIYVYFRPLSMYSVVRDRVATVMYTVVTPMLN  
PFIYSLRNKDMKRGLKKLQDRIYR (SEQ ID NO: 13)

ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACCTGCCCTTTA  
CATCTCTCCCACTGCTTCTCCAAACCCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA  
35 CTACAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCAACCCTCAGCTGCAG  
AAACCTCTCTTTGCCATCTTCTCATCATGTACCTGCTCGCTGCGGTGGGGAATGTGCTCAT  
CATCCCGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACTTTTTTCTCAGCAACT  
TGTCTTTCATGGATATCTGCTTCACAACAGTCATAGTGCCTAAGATGCTGGTGAATTTTCTA  
TCAGAGACAAAGGTTATCTCCTATGTGGGCTGCCTGGCCAGATGTA CTCTTTATGGCAT  
40 TTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCGGCTGGTGGCCATCTG  
CAACCCCTTACACTATGATGTGGTTATGAAACCACGGCATTGCCTGCTCATGCTATTGGGT  
TCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTATGTCTCGCTTGTCTTT  
CTGTGCCTCTCACATCATTAAAGCACTTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT  
GCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTTAGCTGTCATTGTGAC  
45 CCCCTTCTGTGTATCATCTTCTCCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCCT  
CTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCACCTCACTGCAGTAGCCCT  
TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCTGTCCATGTACTCAGTGGTTAGGG  
ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCCTTTCATCTACAG  
CCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAATTTACCGGTA  
50 A (SEQ ID NO: 14)

**AOLFR8 sequences:**

MATSNHSSGAEFILAGLTQRPELQLPLFLFLGIYVTVVGNLGMIFLIALSSQLYPPVYFFLSH  
LSFIDL CYSSVITPKMLVNFVPEENIISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRP LLY  
55 NIVMSHRVCSIMMAVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTLSCSSTHINEI

LLFIIGGVNTLATTLAVLISYAFIFSSILGIHSTEGQSKAFGTCSSHLLAVGIFFGSITFMFKPPSS  
TTMEKEKVSSVFYITIIPMLNPLIYSLRNKDVKNALKKMTRGRQSS (SEQ ID NO: 15)

5 ATGGCTACTTCAAACCAATTCTTCAGGGGCTGAGTTTATCCTGGCAGGCTTGACACAACGCC  
CAGAACTTCAACTGCCACTCTTCCTCCTGTTCTGGAATATATGTGGTCACAGTGGTGGG  
GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTTACCCTCCAGTGTATTATT  
TTCTCAGTCATTTGTCTTTCATTGATCTCTGCTACTCCTCTGTCAATTACCCCTAAGATGCTG  
GTGAACTTTGTTCCAGAGGAGAACATTATCTCCTTTCTGGAATGCATTACTCAACTTTATT  
10 CTTCTTATTTTTGTAATTGCAGAAGGCTACCTTCTGACAGCCATGGAATATGACCGTTAT  
GTTGCTATCTGTCGCCCCTGCTTTACAATATTGTCATGTCCCACAGGGTCTGTTCCATAAT  
GATGGCTGTGGTATACTCACTGGGTTTTCTGTGGGCCACAGTCCATACTACCCGCATGTCA  
GTGTTGTCATTCTGTAGGTCTCATACGGTCAGTCATTATTTTTGTGATATTCTCCCCTTATT  
GACTCTGTCTTGCTCCAGCACCCACATCAATGAGATTCTGCTGTTCAATTATTGGAGGAGTT  
AATACCTTAGCAACTACACTGGCGGTCCTTATCTCTTATGCTTTCAATTTCTCTAGTATCCT  
15 TGGTATTCATTCCACTGAGGGGCAATCCAAAGCCTTTGGCACTTGTAGCTCCCCTCTCTTG  
GCTGTGGGCATCTTTTTTGGGTCTATAACATTTCATGTATTTCAGCCCCCTTCCAGCACTAC  
TATGGAAAAAGAGAAGGTGTCTTCTGTGTTCTACATCACAATAATCCCCATGCTGAATCCT  
CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA  
AGGCAGTCATCCTGA (SEQ ID NO: 16)

20

**AOLFR9 sequences:**

MLARNNSLVTEFILAGLTDRPEFWQPFLLFLVIYIVTMVGNLGLITLFLNSHLHTPMYYFLFN  
LSFIDLCYSSVFTPKMLMNFVSKKNIISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL  
LYKVTMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANIINHYLCDILPLLQLSCTSTYV  
25 NEVVVLIVVGTNITVPSCILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY  
SSGSMEQGVSVFYTNVPMPLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 17)

ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC  
CAGAGTTCTGGCAACCCTTCTTTTTCTGTTCTAGTGATCTACATTGTCACCATGGTAGGC  
30 AACCTTGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT  
CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT  
GAACTTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC  
TTTCTCTTTTTCGTCATCTCTGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT  
GGCCATCTGTAATCCATTGCTGTATAAGGTACCATGTCCCATCAGGTCTGTTCTATGCTCA  
35 CTTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCCACACCGGGTGCATGTTAG  
ACTCACCTTCTGCAGTGCTAATATCATTAACCATTACTTGTGTGACATACTCCCCCTCCTCC  
AGCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTGTGTTCTCATTGTTGTGGGTACTAA  
TATCACGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTCAATTGTCACCTAGCATTCTTC  
ATATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCAATGC  
40 TCTGTCTCTGTTTTTTGGGTGAGCGGCATTATGTATATTAATATTCTTCTGGATCTATGG  
AGCAGGGAAAAAGTTTTTCTGTTTTCTACATAATGTGGTGCCCATGCTCAATCCCTCATC  
TACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTCTAG  
AGGAGAAATATATTCTAA (SEQ ID NO: 18)

45 **AOLFR10 sequences:**

MLARNNSLVTEFILAGLTDRPEFRQPLFFLFLVIYIVTMVGNLGLIILFGLNSHLHTPMYYFLFN  
SFIDLCYSSVFTPKMLMNFVSKKNIISYVGCMTQLFFFLFFVISECYILTSMAYDRYVAICNPLLY  
KVTMSHQVCSMLTFAAYIMGLAGATAHTGCMRLTLFCSANIINHYLCDILPLLQLSCTSTYVN  
EVVVVLIVVGINIMVPSCILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKYS  
50 SGSMEQGVSVFYTNVPMPLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 19)

ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC  
CAGAGTTCCGGCAACCCCTCTTTTTCTGTTCTAGTGATCTACATTGTCACCATGGTAGGC  
AACCTTGCTTGATCATTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT  
55 CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT  
GAACTTTGTATCAAAAAAGAATATTATCTCCTATGTTGGGTGCATGACTCAGCTGTTTTCT

TTCTCTTTTTTGTTCATCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG  
 GCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCAC  
 TTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGCTTAGA  
 CTCACCTTCTGCAGTGCTAATATCATCAACCATTACTTGTGTGACATACTCCCCCTCCTCCA  
 5 GCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTGTGTTCTCATTGTTGTGGGTATTAAT  
 ATCATGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTTCATTGTCACTAGCATTCTTCA  
 TATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCATTGCT  
 CTGCTCTGTTTTTGGGTCAGCGGCATTTCATGTATATTAATAATTCTTCTGGATCTATGGA  
 GCAGGAAAAGTTTCTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCTCTCATCT  
 10 ACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTCAGA  
 GAAGAAATATATTCTAA (SEQ ID NO: 20)

**AOLFR11 sequences:**

MTLRNSSSVTEFILVGLSEQPELQLPLFLLFLGIYVFTVVGNLGLITLIGINPSLHTPMYFFLFNLS  
 15 FIDLCYSCVFTPKMLNDFVSESIISYVGCMTQLFFCFVNSECYVLVSMAYDRYVAICNPLLY  
 MVTMSPRVCFLLMFGSYVVGAFAGAMAHTGSMLRLTFCDNSVIDHYLCDVLPQLSCTSTHV  
 SELVFFIVGVITMLSSISIVISYALILSNILCIPSAEGRSKAFSTWGSIIAVALFFGSGTFTYLTTS  
 FPGSMNHGRFASVFYTNVVPMLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)

20 ATGACTCTGAGAAACAGCTCCTCAGTGACTGAGTTTATCCTTGTGGGATTATCAGAACAGC  
 CAGAGCTCCAGCTCCCTCTTTTCTTCTATTTCTTAGGGATCTATGTGTTCACTGTGGTGGGC  
 AACTTGGGCTTGATCACCTTAATTGGGATAAATCCTAGCCTTCACACCCCCATGTACTTTTT  
 CCTCTTCAACTTGTCTTTATAGATCTCTGTTATTCCTGTGTGTTACCCCCAAAATGCTGA  
 25 TGTTTCTTTGTCAATTCTGAGTGCTATGTGTTGGTATCAATGGCCTATGATCGCTATGTGGC  
 CATCTGCAACCCCTGCTCTACATGGTCACCATGTCCCAAGGGTCTGCTTTCTGCTGATGT  
 TTGGTTCCTATGTGGTAGGGTTTGTGTTGGGCCCATGGCCACACTGGAAGCATGCTGCGACT  
 GACCTTCTGTGATTCCAACGTCATTGACCATTATCTGTGTGACGTTCTCCCCCTCTTGCAGC  
 TCTCCTGCACCAGCACCCATGTCACTGAGCTGGTATTTTTCATTGTTGTTGGAGTAATCACC  
 30 ATGCTATCCAGCATAAGCATCGTCATCTTACGCTTTGATACTCTCCAACATCCTCTGTAT  
 TCCTTCTGCAGAGGGCAGATCCAAAGCCTTTAGCACATGGGGCTCCACATAATTGCTGTT  
 GCTCTGTTTTTTGGGTCAGGGACATTACCTACTTAACAACATCTTTTCTGGCTCTATGAA  
 CCATGGCAGATTTGCCTCAGTCTTTTACACCAATGTGGTTCCTCATGCTTAACCCCTCGATCT  
 ACAGTTTGAGGAATAAGGATGATAAACTTGCCTTGGGCAAAACCCTGAAGAGAGTGCTCT  
 35 TCTAA (SEQ ID NO: 22)

**AOLFR12 sequences:**

MERNHNPDNCNVLNFFEFADKKNKRRNFGQIVSDVGRICYSVLSLGEPTTMGRNNLTRPSEFIL  
 LGLSSRPEDQKPLFAVFLPIYLITVIGNLLILAIRSDTRLQTPMYFFLSILSFVDICYVTVIIPKMLV  
 40 NFLSETKTISYGECLTQMYFFLAFGNTDSYLLAAMADRYVAICNPFHYITIMSHRCCVLLLVLS  
 FCIPHFHSLHLLTNQLIFCASNVIHHFFCDDQPVLKLSCSSHFVKEITVMTEGLAVIMTPFSCIII  
 SYLRILITVLKIPSAAGKRKAFSTCGSHLTVVTLFYGSISYVYFQPLSNYTVKDQIATIIYTVLTP  
 MLNPFYISLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)

45 ATGGAAAGAAACCACAATCCAGATAATTGTAATGTTTTAAATTTTTTCTTTGCTGATAAGA  
 AGAATAAAAGGAGAAATTTTGACAGATTGTATCAGATGTTGGAAGAATCTGTTACAGTG  
 TTAGTTTATCTTTAGGTGAACCCACAACCTATGGGAAGAAATAACCTAACAAGACCCCTGTA  
 ATTCATCCTCCTTGGACTCTCCTCTCGACCTGAGGATCAGAAGCCGCTCTTTGCTGTGTTCC  
 TCCCCATCTACCTTATCACAGTGATAGGAACTGCTTATCATCCTGGCCATCCGCTCAGA  
 50 CACTCGTCTCCAGACGCCATGTACTTCTTCTAAGCATCCTGTCTTTTGTGACATTTGCT  
 ATGTGACAGTCATTATCCCTAAGATGCTGGTGAACCTTCTTATCAGAGACAAAGACCATCTC  
 TTACGGTGAGTGTCTGACCCAGATGTACTTTTTCTTAGCCTTTGGAAACACAGACAGTTAC  
 CTGCTAGCAGCCATGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCACTACATCA  
 CCATTATGAGTCACAGATGCTGTGCTCTGCTTCTGGTCTCTCCTTCTGCATTCCACATTTT  
 55 CACTCCCTCCTGCACATTCTTCTGACTAATCAGCTCATCTTCTGTGCCTCCAATGTCATCCA  
 TCACTTTTTCTGCGATGATCAACCAGTGCTAAAATTGCTCTGTTCTCCCATTTTGTCAAAG

AAATCACAGTAATGACAGAAGGCTTGGCTGTCATAATGACCCCGTTTTTCATGCATCATCAT  
CTCTTATTTAAGAATCCTCATCACTGTTCTGAAGATTCCCTTCAGCTGCTGGAAAGCGTAAA  
GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCCCTGTTTTATGGAAGCATTAGCTA  
TGTCTATTTTCAGCCCCGTGTTCAACTATACTGTCAAGGATCAAATAGCAACAATTATCTAC  
5 ACCGTACTGACTCCTATGCTAAATCCATTATCTATAGTCTGAGGAACAAAGACATGAAGC  
AGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

#### AOLFR13 sequences:

MDQKNGSSFTGFILLGFSRDPQLLELVFVLLIFYIFTLLGNKTIIVLSHLDPHLHNP MYFFFSNL  
10 SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLGSTECVLLGVMAFDRYAAVCRPL  
HYTVVMHPCLYVLMASWSVIGFANSLLQTVLILLTL CGRNKLEHFLCEVPPLLKLACVDTT  
MNESELFVSVIII LPVALIIFSYSQIVRAVVRISATGQRKVFGTCGSHLTVVSLFYGTAIYAY  
LQPGNNYSQDQGXISLFYTIITPMINPLIYTLRNKDKGALKKVLWKYDSR (SEQ ID NO:  
25)

15 ATGGATCAGAAAAATGGAAGTTCTTTCCTACTGGATTATCCTACTGGGTTTCTCTGACAGGC  
CTCAGCTGGAGCTAGTCCTCTTTGTGGTTTCTTTGATCTTCTATATCTTCACTTTGCTGGGG  
AACAAAACCATCATTGTATTATCTCACTGGACCCACATCTTCACAATCCTATGTATTTTTT  
CTTCTCCAACCTAAGCTTTTTGGATCTGTGTACACAACCGGCATTGTTCCACAGCTCCTGG  
20 TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGTAGTTCAGCTGTACAT  
CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTGACCGCTAT  
GCAGCTGTTTGCAGGCCCCCTCCACTACACAGTAGTCATGCACCTTGTCTGTATGTGCTGA  
TGGCTTCTACTTCATGGGTCATTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTG  
CTTTTAACACTTTGTGGAAGAAATAAATTAGAACACTTTCTTTGTGAGGTTCTCCATTGCT  
25 CAAGCTTGCCTGTGTTGACACTACTATGAATGAATCTGAACTCTTCTTTGTGAGTGTCTATTA  
TTCTTCTTGTACCTGTTGCATTAATCATATTCTCCTATAGTCAGATTGTGAGGGCAGTCGTG  
AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTGTTGGGACATGTGGCTCCACCTCACA  
GTGGTTTCCCTGTTCTACGGCACAGCTATCTATGCTTACCTCCAGCCCGGCAACAACACTCTC  
TCAGGATCAGGGCAAGKTCATCTCTCTCTTCTACACCATCATTACACCCATGATCAACCCC  
30 CTCATATATACACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG  
AACTACGACTCCAGATGA (SEQ ID NO: 26)

#### AOLFR14 sequences:

MALPLLLSPSCFASSQSLSSRMNSENLTRAAVAPAEFVLLGITNRWDLRVALFLTCLPVYLVSL  
35 LGNMGMALLIRMDARLHTPMYFFLANLSLLDACYSIAIGPKMLVDLLLPRATIPYTACALQMF  
VFAGLADTECCLLAAMAYDRYVAIRNPLLYTTAMSQRLCLALLGASGLGGAVSAFVHTTLTF  
RLSFCRSRKINSFFCDIPLLAISCDTSLNELLFAICGFIQTATVLAITVSYGFIAGAVIHMRSE  
GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSSYALD TDKMASVFYTLVIPSLNPLIYSLRNKE  
VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

40 ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCTCTTCTCAGTCTCTGTCCAGTAG  
GATGAACTCAGAGAACCTCACCCGGGGCCGCGGTTGCCCTGCTGAATTCGTCCTCCTGGGG  
ATCACAATCGCTGGGACCTGCGTGTGGCCCTCTCCTGACCTGCCTGCCTGTCTACCTGG  
TGAGCCTGCTGGGAAACATGGGCATGGCGCTGCTGATCCGCATGGATGCCCGGCTCCACA  
45 CACCTATGTACTTCTTCTGCGCAACCTCTCCCTGCTGGATGCCTGCTATTCTCCGCCATC  
GGCCCCAAGATGCTAGTGACCTGCTGCTGCCCGGAGCCACCATCCCTTACACAGCCTGTG  
CCCTCCAGATGTTTGTCTTTGCAGGTCTGGCTGATACTGAGTGTGCTTGTGCTGGCAGCCAT  
GGCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATACAACAGCTATGTGCGAG  
CGTCTATGCCTGGCCTTGTGCTGGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGCTTTGTTT  
50 ACACAACCCTCACCTTCCGCTGAGCTTCTGCGCTCCCGGAAGATCAATAGCTTCTTCTG  
CGATATCCCTCCACTGCTGGCCATCTCGTGCAGTGACACCAGTCTCAATGAACTCCTTCTCT  
TCGCCATCTGTGGCTTCATCCAGACAGCCACGGTGTTAGCTATCACGGTGTCTTATGGCTT  
CATCGCTGGGGCTGTGATCCACATGCGCTCGGTGAGGGCAGTCGCGGAGCAGCCTCCAC  
CGGTGTTTCCACCTCACAGCCGTGGCCATGATGTACGGGACACTCATTTTCATGTACCTG  
55 CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCCTGG

TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT  
CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGGTCCCAGTGA (SEQ ID NO: 28)

**AOLFR15 sequences:**

5 MRENNQSSSTLEFILLGVTGQQEQEDFFYILFLFIYPITLIGNLLIVLAICSDVRLHNP MYFLLANLS  
LVDIFFSSVTIPKMLANHLLGSKSISFGGCLTQMYFMIALGNTDSYILAAMAYDRAVAISHPLH  
YTTIMSPRSCIWLIAGSWVIGNANALPHTLLTASLSFCGNQEVANFYCDITPLLKLS CSDIHFHV  
KMMYLGVGIFSVPLLCHVSYIRVFSTVFQVPSTKGVLKAFSTCGSHLTVVSLYYGTVMGTYFR  
PLTNYSLKDAVITVMYTAVTPMLNPFYSLRNRDMKAALRKLFNKRISS (SEQ ID NO: 29)

10

ATGAGGGAAAAATAACCAGTCCTCTACACTGGAATTCATCCTCCTGGGAGTTACTGGTCAGC  
AGGAACAGGAAGATTTCTTCTACATCCTCTTCCTGTTCATTTACCCCATCACATTGATTGGA  
AACCTGCTCATTGTCCTAGCCATTTGCTCTGATGTTTCGCCTTCACAACCCCATGTATTTCT  
CCTTGCCAACCTCTCCTTGGTTGACATCTTCTCTCATCGGTAACCATCCCTAAGATGCTGG  
15 CCAACCATCTCTTGGGCAGCAAATCCATCTCTTTTGGGGGATGCCTAACGCAGATGTATTT  
CATGATAGCCTTGGGTAACACAGACAGCTATATTTGGCTGCAATGGCATATGATCGAGCT  
GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTCCACGGTCTTGTATCTGGC  
TTATTGCTGGGTCTTGGGTGATTGGAAATGCCAATGCCCTCCCCCACACTCTGCTCACAGC  
TAGTCTGTCCCTTCTGTGGCAACCAGGAAGTGGCCAACCTTCTACTGTGACATTACCCCTTG  
20 CTGAAGTTATCCTGTTCTGACATCCACTTTCATGTGAAGATGATGTACCTAGGGGTTGGCA  
TTTTCTCTGTGCCATTACTATGCATCATTGTCTCCTATATTCGAGTCTTCTCCACAGTCTTCC  
AGGTTCCCTCCACCAAGGGCGTGCTCAAGGCCTTCTCCACCTGTGGTTCCACCTCACGGT  
TGTCTCTTTGTATTATGGTACAGTCATGGGCACGTATTTCGCCCTTTGACCAATTATAGCC  
TAAAAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTAAATCCTTTTCAT  
25 CTACAGTCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAAACTCTTCAACAAGAGAAT  
CTCCTCGTAA (SEQ ID NO: 30)

**AOLFR16 sequences:**

30 MRRNCTLVTEFILLGLTSRRELQILLFTLFLAIYMTVAGNLGMIVLIQANAWLHMP MYFFLSH  
LSFVDLCFSSNVTPKMLEIFLSEKKSISYPACLVCYLFIALVHVEIYILAVMAFD RYMAICNPLL  
YGS RMSKSVCSFLITVPYVYGALTGLMETMWTYNLAF CGPNEINH FYCADPPLIKLACSDTYN  
KELSMFIVAGWNLSFSLFIICISYLYIFPAILKIRSTEGRQKAFSTCGSHLTAVTIFYATLFFMYLR  
PPSKESVEQGKMVAVFYTTVIPMLNLIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

35 ATGAGAAGAAACTGCACGTTGGTGACTGAGTTCATTCTCCTGGGACTGACCAGTCGCCGG  
GAATTACAAATTCTCCTCTTCACGCTGTTTCTGGCCATTTACATGGTCACGGTGGCAGGGA  
ACCTTGGCATGATTGTCCTCATCCAGGCCAACGCTGGCTCCACATGCCATGTACTTTTTC  
CTGAGCCACTTATCCTTCGTGGATCTGTGCTTCTCTTCCAATGTGACTCCAAAGATGCTGG  
AGATTTTCTCTTTCAGAGAAGAAAAGCATTTCCTATCCTGCCTGTCTTGTGCAGTGTTACCTT  
40 TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGGCCTTTGACCGGTACAT  
GGCCATCTGCAACCCTCTGCTTTATGGCAGCAGAATGTCCAAGAGTGTGTGCTCCTTCCTC  
ATCAGGTGCCTTATGTGTATGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA  
ACCTAGCCTTCTGTGGCCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCACTGAT  
TAAGCTGGCTTGTCTGACACCTACAACAAGGAGTTGTCAATGTTTATTGTGGCTGGCTGG  
45 AACCTTCTTTTTCTCTCTTCATCATATGTATTTCTACCTTTACATTTTCCCTGCTATTTTA  
AAGATTCTGCTCTACAGAGGGCAGGCAAAAAGCTTTTTCTACCTGTGGCTCCCATCTGACAG  
CTGTCACTATATTCTATGCAACCCTTTTCTTCATGTATCTCAGACCCCCCTCAAAGGAATCT  
GTTGAACAGGGTAAAATGGTAGCTGTATTTTATACCACAGTAATCCCTATGCTGAACCTTA  
TAATTTATAGCCTTAGAAATAAAAATGTAAAAGAAGCATTAAATCAAAGAGCTGTCAATGA  
50 AGATATACTTTTCTTAA (SEQ ID NO: 32)

**AOLFR17 sequences:**

55 MLNFTDVTEFILLGLTSRREWQVLFFIIFLVVYIITMVG NIGMMVLIKVSPQLNNP MYFFLSHLS  
FVDVWFSSNVTPKMLENLFSDKKTITYAGCLVQCFFFIALVHVEIFILAAMAFDRYMAIGNPLL  
YGS KM SRVVCIRLITFPYIYGFLTSLAATLW TYGLYFCGKIEINH FYCADPPLIKMACAGTFVKE

YTMILAGINFTYSLTVIIISYLFILAILMRMSAEGRQKAFSTCGSHLTAVIIFYGTLIFMYLRRPTE  
ESVEQGKMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

5 ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGAGAAT  
GGCAAGTTCTCTTCTTCATCATCTTTCTGTGGTCTACATCATCACCATGGTGGGCAATATC  
GGCATGATGGTGTTAATCAAGGTCAGTCCTCAGCTTAACAACCCCATGTACTTTTCTCTCA  
GTCACCTGTCAATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGAAAAAC  
CTGTTTTTCAGATAAAAAACAATTACTTATGCTGGTTGTTTAGTACAGTGTTTCTTCTTCAT  
10 TGCTCTTGCCATGTGGAATTTTTATTCTTGCTGCGATGGCCTTTGATAGATACATGGCAA  
TTGGGAATCCTCTGCTTTATGGCAGTAAAATGTCAAGGGTTGTCTGTATTTCGACTGATTAC  
TTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTGT  
ACTTCTGTGAAAAATTGAGATCAACCATTCTACTGTGCAGATCCACCTCTCATCAAAAT  
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGATCATACTTGCCGGCATTAACTTC  
ACATATTCCCTGACTGTAATTATCATCTTACTTATTATCCTCATTGCCATTCTGCGAAT  
15 GCGCTCAGCAGAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCCTCTGACAGCTGT  
CATTATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG  
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA  
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT  
GTAA (SEQ ID NO: 34)

20

**AOLFR18 sequences:**

MSNTNGSAITEFILLGLTDCPELQSLFLVLFLVVYLVTLGNLGMIMLMRLDSRLHTPMYFFLT  
NLAFLVLCYTSNATPQMSTNIVSEKTISFAGCFTQCYIFIALLLTEFYMLAAMAYDRYVAIYDP  
LRYSVKTSRRVCICLATFPYVYGFSDFLQAILTFRLTFCRSNVINHFYCADPPLIKLSCSDTYVK  
25 EHAMFISAGFNLSSSLTIVLVSYAFILAILRIKSAEGRHKAFSTCGSHMMAVTLFYGTLFCMYI  
RPPTDKTVEESKIIAVFYTFVSPVLNPLIYSLRNKDVQALKNVLR (SEQ ID NO: 35)

30 ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC  
CGAACTCCAGTCTCTGCTTTTTGTGCTGTTTCTGGTTGTTTACCTCGTCACCCCTGCTAGGC  
AACCTGGGCATGATAATGTTAATGAGACTGGACTCTCGCCTTCACACGCCCATGTACTTCT  
TCCTCACTAACTTAGCCTTTGTGGATTTGTGCTATACATCAAATGCAACCCCGCAGATGTC  
GACTAATATCGTATCTGAGAAGACCATTTCCTTTGCTGGTTGCTTTACACAGTGCTACATTT  
TCATTGCCCTTCTACTCACTGAGTTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT  
GGCCATATATGACCCTCTGCGCTACAGTGTGAAAACGTCCAGGAGAGTTTGCATCTGCTTG  
35 GCCACATTTCCCTATGTCTATGGCTTCTCAGATGGACTCTTCCAGGCCATCCTGACCTTCCG  
CCTGACCTTCTGTAGATCCAATGTCATCAACCACTTCTACTGTGCTGACCCGCCGCTCATT  
AGCTTTCTTGTTCTGATACTTATGTCAAAGAGCATGCCATGTTTCATATCTGCTGGCTTCAAC  
CTCTCCAGCTCCCTCACCATCGTCTTGGTGTCTTATGCCTTCATTCTTGCTGCCATCCTCCG  
GATCAAATCAGCAGAGGGAAGGCACAAGGCATTCTCCACCTGTGGTTCCCATATGATGGC  
40 TGTCACCTGTGTTTATGGGACTCTCTTTGCATGTATATAAGACCACCAACAGATAAGACT  
GTTGAGGAATCTAAAATAAGCTGTCTTTTACACCTTTGTGAGTCCGGTACTTAATCCAT  
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTTGAAGAATGTCCTGAGATGA  
(SEQ ID NO: 36)

45 **AOLFR19 sequences:**

METKNYSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLTAVGNVLILAIYSDPRLHTPMYFFLSNL  
SFMDICFTTVIVPKMLVNFLSETKIISYVGCLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH  
YDVVMKPWHCLLMLLGSCSISHLHSLFRVLLMSRSLFCASHIHKHFFCDTQPVCLKSCSDTSSSQ  
MVVMTETLAVIVTPFLCTIFSYLQIIVTVLRIPSAAGKWKAFTSCGSHLTVVVLFYGSVIYVYFR  
50 PLSMYSVMKGRVATVMYTVVTPMLNPMFIYSLRNKDMKRGLKLRHRIYS (SEQ ID NO: 37)

ATGGAGACAAAGAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCA  
ACCTAAGCTGCAGAAACCTCTCTTTGCCATCTTCTCATCATGTACCTACTCACTGCGGTG  
GGGAATGTGCTCATCATCCTGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACT  
55 TTTTCTCAGCAACTTGCTTTTCATGGATATCTGCTTCAACAACAGTCATAGTCCTAAGATG  
CTGGTGAATTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT

ACTTCTTCATGGCATTGTTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG  
 GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA  
 CTCATGCTATTGGGTTCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTAT  
 GTCTCGCTTGTCTTTCTGTGCCTCTCACATCATTAAAGCACTTTTTCTGTGACACCCAGCCTG  
 5 TGCTAAAGCTCTCCTGCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGAGCCTT  
 AGCTGTCATTGTGACCCCTTCTGTGTACCATCTTCTCCTACCTGCAAATCATCGTCACTG  
 TGCTCAGAAATCCCTCTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCACCT  
 CACTGTAGTGGTCTGTTCTATGGGAGTGTCTATGTCTATTTTAGGCCTCTGTCCATGT  
 10 ACTCAGTGATGAAGGGCCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGA  
 ACCCTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTTGAAGAAATTAAGAC  
 ACAGAATTTACTCATAG (SEQ ID NO: 38)

#### AOLFR20 sequences:

MVEENHTMKNEFILTGFTDHPKLTLLFVVFVFAIYLITVVGNISLVALIFTHCRLHTPMYIFLGN  
 15 LALVDSCCACAITPKMLENFFSEGKRISLYECAVQFYFLCTVETADCFLLAAVAYDRYVAICNP  
 LQYHIMMSKKLCIQMTTGAFIAGNLHSMIHVGLVFRLLVFCGLNHINHFYCDTLPYRLSCVDPF  
 INELVLFIFSGSVQVFTIGSVLISLYILLTIFRMSKEGRAKAFSTCASHFSSVSLFYGSIFFLYIRP  
 NLLEGGNDIPAILFTIVVPLNPFYSLRNKEVISVLRKILLKIKSQGSVNK (SEQ ID NO: 39)

20 ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTTATCCTCACAGGATTTACAGATCACC  
 CTGAGCTGAAGACTCTGCTGTTTGTGGTGTCTTTGCCATCTATCTGATCACCCTGGTGGG  
 GAATATTAGTTTGGTGGCACTGATATTTACACACTGTCGGCTTCACACACCAATGTACATC  
 TTTCTGGGAAATCTGGCTCTTGTGGATTCTTGTCTGTGCCTGTGCTATTACCCCCAAAATGTT  
 AGAGAACTTCTTTCTGAGGGCAAAAGGATTTCCCTCTATGAATGTGCAGTACAGTTTTAT  
 25 TTTCTTTGCACTGTGGAACTGCAGACTGCTTTCTTCTGGCAGCAGTGGCCTATGACCGCT  
 ATGTGGCCATCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAACTCTGCATTCA  
 GATGACCACAGGCGCCTTCATAGCTGGAATCTGCATTCCATGATTTCATGTAGGGCTTGTA  
 TTTAGGTTAGTTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATACTCTTCCCTT  
 GTATAGACTCTCCTGTGTTGACCCTTTCATCAATGAACTGGTTCTATTTCATCTTCTCAGGT  
 30 CAGTTCAAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTATATTCTTCTTACTATT  
 TTCAGAATGAAATCCAAGGAGGGAAGGGCCAAAGCCTTTTCTACTTGTGCATCCCACTTTT  
 CATCAGTTTCATTATTCTATGGATCTATTTTTTCTTATACATTAGACCAAATTTGCTTGAA  
 GAAGGAGGTAATGATATACCAGCTGCTATTTTATTACAATAGTAGTTCCCTTACTAAATC  
 CTTTCATTTATAGTCTGAGAAACAAGGAAGTAATAAGTGTCTTAAGAAAAATTCTGCTGAA  
 35 AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

#### AOLFR21 sequences:

MEPRKNVTDVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVVTVTVSETLGSPMSFFLAGL  
 40 TFDIIYSSSISPRLLISDLFFGNNSISFQSFMAQLFIEHLFGGSEVFLLLVMAVDRYVAICKPLHYLV  
 IMRQWVCVLLLVSWSVGGFLQSVFQLSHYGLPFCGPNVIDHFFCDMYPLLKLACTDTHVIGLL  
 VVANGGLSCTIAFLLLLISYGVILHSLKKLSQKGRQKAHSTCSSHITVVVFFVPCIFMCARPAR  
 TFSIDKSVSVFYTVITPMLNPLIYTLRNSEMTSAMKKL (SEQ ID NO: 41)

45 ATGGAGCCAAGGAAAAATGTGACTGACTTTGTCTCTTGGGCTTCACACAGAATCCAAAG  
 GAGCAGAAAGTACTTTTTGTTATGTTCTTGTCTTCTACATTTTGACCATGGTGGGCAACCT  
 GCTCATTGTAGTGACCGTAACTGTCAGTGAGACCCTGGGCTCACCAATGTCCTTCTTTCTT  
 GCTGGCTTAACATTTATAGATATCATTTATTCTTCATCCATTTCCCCCAGATTGATTTGAGA  
 CTTGTTCTTTGGGAATAATTCCATATCCTTCCAATCTTTCATGGCCCAGCTCTTTATCGAGC  
 50 ACCTTTTGGTGGGTGAGAGGTCTTCTCCTTGGTGATGGCCTATGACCGCTATGTGGC  
 CATCTGTAAGCCCTTGCAATTATTGGTTATCATGAGACAATGGGTGTGTGTTTTGCTGCTG  
 GTAGTGTCTGGGTTGGAGGATTTCTGCAATCAGTATTTCAACTTAGCATTATTTATGGGC  
 TCCCATTCTGTGGCCCCAATGTCATTGATCATTTTTTCTGTGACATGTATCCCTTATTGAAA  
 CTGGCCTGCACTGACACCCATGTTATTGGCCTCTTAGTGGTGGCCAATGGAGGACTGTCTT  
 GCACTATTGCGTTTCTGCTCTTACTCATCTCTTATGGTGTCTCCTGCACTCTCTAAAGAAA  
 55 CTTAGTCAGAAAGGGAGGCAAAAAGCCCACTCAACCTGCAGTCCACATCACTGTGGTTG  
 TCTTCTTCTTTGTTCTTGTATTTTATGTGTGCTAGACCTGCTAGGACCTTCTCCATTGAC



AAATCAGTGAGTGTGTTTTATACAGTCATAACCCCAATGCTGAACCCCTTAATCTACACTC  
TGAGAAATTCTGAGATGACAAGTGCTATGAAGAAGCTTTAG (SEQ ID NO: 42)

**AOLFR22 sequences:**

5 MRXXNXXTEFVLLGFSQDPGVXKALFVMFLITYXXTVVGNLLIVVDIIASPLGSPMYFFLAC  
LSFIDAAYSTTISPKLIVGLFCDKKTISFQGCMGQLFIDHFFGGAEVFLLVVMACDRYVAICKPL  
HYLTIMNRQVCFLLLVXXMIGGFVHSAFQIVVYSLPFCGPXVIVHFSCDMHPLLELACTDITYFI  
GLTVVNSGAICMVIFNLLISYGVILSSLKTYSQEKRKALSTCSSGSTVVVLFVPCIFIYVRP  
VSNFPTDKFMTVFYTIITHMLSPLIYTLRNSEMRNAIEKLLGKKLTIFIIGGVSVLM (SEQ ID NO:  
10 43)

ATGAGACANNNAACAATATNACAGAATTTGTCCTCCTGGGCTTTTCTCAGGATCCTGGTG  
TGNNNAAAGCATTATTTGTCATGTTTTTACTCACATACNNNNNNACAGTGGTGGGGAACCT  
GCTCATTGTNGTGGATATTATTGCCAGCCCTTNNTTGGGTTCCTCAATGTATTTCTTCCTTG  
15 CCTGCCTGTCATTTATAGATGCTGCATATTCCACTACCATTTCTCCCAAGTTAATTGTAGGC  
TTATTCTGTGATAAAAAGACTATTTCTTCCAAGGTTGCATGGGCCAGCTATTTATAGACC  
ATTTCTTTGGTGGGGCTGAGGTCTTCTTCTGGTGGTGATGGCCTGTGATCGCTATGTGGC  
CATCTGTAAGCCACTGCACTATTTGACCATCATGAATCGACAGGTTTGCTTCTTCTGTTGG  
TNNTNNCCATGATTGGAGGTTTTGTACATTCTGCGTTTCAAATTGTTGTGTACAGTCTCCCT  
20 TTCTGTGGTCCCNATGTCATTGTTTCACTTGTGACATGCACCCATTACTGGAACCTGGC  
ATGCACTGACACCTACTTTATAGGCCTCACTGTTGTTGTCAATAGTGGAGCAATCTGTATG  
GTCATTTTCAACCTTCTGTTAATCTCCTATGGAGTCATCCTAAGCTCCCTTAAACCTTACAG  
TCAGGAAAAGAGGGGTAAAGCCTTGTCTACCTGCAGCTCCGGCAGTACCGTTGTTGTCTCT  
TTTTTGTACCCTGTATTTTCATATATGTTAGACCTGTTTCAAACCTTCTACTGATAAGTT  
25 CATGACTGTGTTTTATACCATTATCACACACATGCTGAGTCCTTTAATATATACGTTGAGA  
AATTCAGAGATGAGAAATGCTATAGAAAACTCTTGGGTAAAAAGTAACTATATTTATTA  
TAGGAGGAGTGTCCGTCCTCATGTAG (SEQ ID NO: 44)

**AOLFR23 sequences:**

30 MAKNNLTRVTEFILMGFMDHPKLEIPLFLVFLSFYLVTLGNVGMIMLIQVDVKLYTPMYFFLS  
HLSLLDACYTSVITPQILATLATGKTVISYGHCAAQFFLTICAGTECFLLAVMAYDRYAAIRNP  
LLYTVAMNPRLCWSLVVGAYVCGVSGAILRTTCTFTLSFCKDNQINFFCDLPPLKLACSDTA  
NIEIUIFFGNFVILANASVILISYLLIKTILKVKSSGGRAKTFSTCASHITAVALLFGALIFMYLQS  
GSGKSLEEDKVVSFVYTVVIPMLNPLIYSLRNKDVKDAFRKVARRLQVSLSM (SEQ ID NO: 45)

35 ATGGCCAAGAATAATCTCACCAGAGTAACCGAATTCATTCTCATGGGCTTTATGGACCACC  
CCAAATTGGAGATTTCCCTCTTTCTGGTGTCTTCTGAGTTTCTACCTAGTCACCTTCTTGGG  
AATGTGGGGATGATTATGTTAATCCAAGTAGATGTCAAACCTACACCCCAATGTACTTCT  
TCCTGAGCCACCTCTCCCTGCTGGATGCCTGTTACACCTCAGTCATCACCCCTCAGATCCTA  
40 GCCACATTGGCCACAGGCAAAACGGTCATCTCTACGGCCACTGTGCTGCCAGTTCTTTT  
TATTCACCATCTGTGCAGGCACAGAGTGCTTTCTGCTGGCAGTGATGGCCTATGATCGCTA  
TGCTGCCATTGCAACCCACTGCTCTATACCGTGGCCATGAATCCCAGGCTCTGCTGGAGC  
CTGGTGGTAGGAGCCTATGTCTGTGGGGTGTGAGGAGCCATCCTGCGTACCACTTGACCT  
TCACCTCTCCTTCTGTAAGGACAATCAAATAAACTTCTTCTTCTGTGACCTCCCACCCCTG  
45 CTGAAGCTTGCCTGCAGTGACACAGCAAACATCGAGATTGTGTCATCATCTTCTTTGGCAATT  
TTGTGATTTTGGCCAATGCCTCCGTCATCCTGATTTCTATCTGCTCATCATCAAGACCATT  
TTGAAAGTGAAGTCTTCAGGTGGCAGGGCCAAGACTTTCTCCACATGTGCCTCTCACATCA  
CTGCTGTGGCCCTTTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAAGTGGCTCAGGCAA  
TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCATCCCCGTGCTGAACC  
50 CTCTGATCTACAGCTTAAGAAACAAAGATGTAAAGACGCCTTCAGAAAGGTCGCTAGGA  
GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

**AOLFR25 sequences:**

55 METGNLTWVSDFVFLGLSQTRELQRFLFVYITTVMGNILIITVTSDSLHTPMYFLLRN  
LAVLDLCFSSVTAPKMLVDLLSEKKTISYQGCMMQIFFHFLGGAMVFFLSVMAFDRLIAISRPL  
RYVTVMNTQLWVGLVAVTWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVRLACTDT

SLLEFLKISNSGLLDVWVFFLLMSYLFILVMLRSHPGEARRKAASCTTHIIVVSMIFVPSIYLY  
ARPFTPFPMDKLV SIGHTVMTPLNPMIYTLRNQDMQAAVRRLGRHRLV (SEQ ID NO: 47)

5 ATGGAACAGGGAACCTCACGTGGGTATCAGACTTTGTCTTCCTGGGGCTCTCGCAGACTC  
GGGAGCTCCAGCGTTTCCTGTTTCTAATGTTCCCTGTTTGTCTACATCACCAGTGTATGGGA  
AACATCCTTATCATCATCAGTGACCTCTGATTCCCAGCTCCACACACCCATGTACTTTCT  
GCTCCGAAACCTGGCTGTCCTAGACCTCTGTTTCTCTTCAGTCACTGCTCCCAAATGCTAG  
TGGACCTCCTCTCTGAGAAGAAAACCATCTCTTACCAGGGCTGCATGGGTGAGATCTTCTT  
CTTCCACTTTTTGGGAGGTGCCATGGTCTTCTTCCTCTCAGTGATGGCCTTTGACCGCCTCA  
10 TTGCCATCTCCCGGCCCTCCGCTATGTACCGTCATGAACACTCAGCTCTGGGTGGGGCT  
GGTGGTAGCCACCTGGGTGGGAGGCTTTGTCCACTCTATTGTCCAGCTGGCTCTGATGCTC  
CCACTGCCCTTCTGTGGCCCCAACATTTGGATAACTTCTACTGTGATGTTCCCAAGTACT  
GAGACTTGCTGCACTGACACCTCACTGCTGGAGTTCCTCAAGATCTCCAACAGTGGGCTG  
CTGGATGTCGTCTGGTCTTCTCCTCCTGATGTCCTACTTATTCATCCTGGTGATGCTGAG  
15 GTCACATCCAGGGGAGGCAAGAAGGAAGGCAGCTTCCACCTGCACCACCCACATCATCGT  
GGTTTCCATGATCTTCGTTCCAAGCATTTACCTCTATGCCCGGCCCTTCACTCCATTCCCTA  
TGGACAAGCTTGTGTCCATCGGCCACACAGTCATGACCCCCATGCTCAACCCCATGATCTA  
TACCCTGAGGAACAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT  
TTGA (SEQ ID NO: 48)

20

**AOLFR26 sequences:**

MAAKNSSVTEFILEGLTHQPGLRIPLFFLFLGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLNL  
LIDFCSTTTITPKMLMSFVSRKNIISFTGCMTQLFFCFVSVESFILSAMAYDRYVAICNPLLYT  
VTMSQVCLLLLLGAYGMGFAGAMAHTGSIMNLTFCADNLVNHFMCDILPPELSCNSSYMN  
25 ELVVFIVAVDVGMPIVTVFISYALILSSILHNSSTEGRSKAFSTCSSHIIVVSLFFGSGAFMYLKP  
LSILPLEQGVSSLFYTHIVPVLNPLIYSLRNKDKVALRRTLGRKIFS (SEQ ID NO: 49)

ATGGCAGCCAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGG  
GACTGCGGATCCCCCTCTTCTTCCTGTTTCTGGGTTTCTACACGGTCACCGTGGTGGGGAA  
30 CCTGGGCTTGATAACCTGATTGGGCTGAACCTCAGCTGCACTCCCATGTACTTCTTCC  
TTTTTAACCTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAAATGCTGATG  
AGTTTTGTCTCAAGGAAGAACATCATTTCTTCACAGGGTGTATGACTCAGCTCTTCTTCTT  
CTGCTTCTTTGTCTCTCTGAGTCCTTCATCCTGTGAGCGATGGCGTATGACCGCTACGTGG  
CCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTGCTCCTTTTG  
35 TTGGGTGCCTATGGGATGGGGTTTGCTGGGGCCATGGCCACACAGGAAGCATAATGAAC  
CTGACCTTCTGTGCTGACAACCTTGTCAATCATTTGATGTGTGACATCCTTCTCTCCTTGA  
GCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTGGTGGCTGTTGAC  
GTTGGAATGCCCATGTGCACTGTCTTTATTTCTTATGCCCTCATCCTCTCCAGCATTCTACA  
CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCAAGTCCCACATAATTGTA  
40 GTTTCTCTTTTCTTTGGTTCTGGTGCTTTTATGTATCTCAAACCCCTTTCCATCCTGCCCCCTC  
GAGCAAGGGAAAGTGTCTCCTGTTCTATACCATAATAGTCCCGTGTTAAACCCATTAA  
TCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGGAGAACTTTGGGCAGAAAAA  
TCTTTTCTTAA (SEQ ID NO: 50)

45 **AOLFR27 sequences:**

MPSQNYSIIEFNLFGFSAFPQHLLPILFLLYLLMFLFTLLGNLLIMATIWIEHRLHTPMYFLCTL  
SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFGFTHSFLLLVMGYDRYVAICHPLR  
YNVLMSPRCAHLVACTWAGGSVMGMMVTTIVFHLTFCSNVIIHFFCHVLSLLKLACENKT  
SSVIMGVMLVCVTALIGCLFLILSYVFIVAAILRIPSAEGRHKTFSTCVSHLTVVVTHYSFASFIY  
50 LKPKGLHSMYSDALMATYTVFTPFSLPIIFSLRNKELKNAINKNFYRKFCPPSS (SEQ ID NO:  
51)

ATGCCTAGTCAGAACTATAGCATCATATCTGAATTTAACCTCTTTGGCTTCTCAGCCTTCCC  
CCAGCACCTCCTGCCATCTTGTTCCTGCTGTACCTCCTGATGTTCTGTTACATTGCTGG  
55 GCAACCTTCTCATCATGGCCACAATCTGGATTGAACACAGACTCCACACACCCATGTACCT  
CTTCTGTGCACCTCTCCGTCTCTGAGATTCTGTTCACTGTTGCCATCACCCCTCGCATGC

TGGCTGATCTGCTTTCCACCCATCATTCCATCACCTTTGTGGCTTGTGCCAACCAGATGTTCT  
 TTCTCCTTCATGTTTGGCTTCACTCACTCCTTCCTTCTCCTGGTCATGGGCTATGATCGCTA  
 TGTGGCCATCTGCCACCCACTGCGTTACAATGTGCTCATGAGCCCCCGTGACTGTGCCCAT  
 CTTGTGGCCTGTACCTGGGCTGGTGGCTCAGTCATGGGGATGATGGTGACAACGATAGTTT  
 5 TCCACCTCACTTTCTGTGGGTCTAATGTGATCCACCATTCTTCTGTTCATGTGCTTTCCCTCT  
 TGAAGTTGGCCTGTGAAAACAAGACATCATCTGTCATCATGGGTGTGATGCTGGTGTGTGT  
 CACAGCCCTGATAGGCTGTTTATTCCTCATCATCCTCTCCTATGTCTTCATTGTGGCTGCCA  
 TCTTGAGGATTCCCTCTGCCGAAGGCCGGCACAAGACATTTTCTACGTGTGTATCCACCT  
 CACTGTGGTGGTCACGCACTATAGTTTTGCCTCCTTTATCTACCTCAAGCCCAAGGGCCTCC  
 10 ATTCTATGTACAGTGACGCCTTGATGGCCACCACCTATACTGTCTTCACCCCTTCCTTAGC  
 CCAATCATTTTCAGCCTAAGGAACAAGGAGCTGAAGAATGCCATAAATAAAAACTTTTACA  
 GAAAATTCTGTCTCCAAGTTCCTGA (SEQ ID NO: 52)

**AOLFR28 sequences:**

15 MPNFTDVTEFTLLGLTCRQELQVLFFVFLAVYMITLLGNIGMILISISPQLQSPMYFFLSHLSF  
 ADVCFSSNVTPKMLENLLSEKTIISYVGCLVQCYFFIAVHVHVEVYLAVMAFDHYMAGCXPL  
 YGSKMSRTVCVRLISVXYXYGFSVSLICTLWYGLYFCGNFEINHFYCADPPLIQLACGRVHIKE  
 ITMIVIAGINFTYSLSVVLISYTLIVVAVLRMRSADGRRKAFSTCGSHLTAVSMFYGTPIFMYLR  
 RPTESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKEAVNKAITKTYVRQ (SEQ ID NO: 53)  
 20  
 ATGCCTAATTTACGGATGTGACAGAATTTACTCTCCTGGGGCTGACCTGTCGTCAGGAGC  
 TACAGGTTCTCTTTTTTGTGGTGTTCCTAGCGGTTTACATGATCACTCTGTTGGGAAATATT  
 GGTATGATCATTTTGATTAGCATCAGTCCTCAGCTTCAGAGTCCCATGTACTTTTCTGAG  
 TCATCTGTCTTTTGGCGACGTGTGCTTCTCCTCCAACGTTACCCCCAAAATGCTGGAAGAACT  
 25 TATTATCAGAGACAAAACCATTTCTATGTGGGATGCTTGGTGCAGTGCTACTTTTTCAT  
 TGCCGTTGTCCACGTGGAGGTCTATATCCTGGCTGTGATGGCCTTTGACAGGTACATGGCC  
 GGCTGCAANCTCTGCTTTATGGCAGTAAATGTCTAGGACTGTGTGTGTGTCGGCTCATCT  
 CTGTGNNNTATGNNNTATGGATTCTCTGTGAGCCTAATATGCACACTATGGACTTATGGCTT  
 ATACTTCTGTGGAACTTTGAAATCAATCACTTCTATTGTGCAGATCCCCCTCTCATCCAGA  
 30 TTGCCTGTGGGAGAGTGCACATCAAAGAAATCACAATGATTGTTATTGCTGGAATTAACCT  
 CACATATTCCTCTCGGTGGTCTCATCTCCTACACTCTCATTGTAGTAGCTGTGCTACGCA  
 TGGCTCTGCCGATGGCAGGAGGAAGGCGTTCTCCACCTGTGGGTCCCACTTGACGGCTGT  
 TTCTATGTTTTATGGGACCCCCATCTTCATGTATCTCAGGAGACCCACTGAGGAATCCGTA  
 GAGCAGGGCAAAATGGTGGCTGTGTTTTACACCACAGTAATTCCTATGTTGAATCCCATGA  
 35 TCTACAGTCTGAGAAATAAGGATGTAAAGAAGCAGTCAACAAAGCAATCACCAAGACAT  
 ATGTGAGGCAGTAA (SEQ ID NO: 54)

**AOLFR29 sequences:**

40 MMSFAPNASHSPVFLLLGFSRANISYTLFFFLAIYLTILGNVTLVLLISWDSRLHSPMYYLLR  
 GLSVIDMGLSTVTLPLQLLAHLVSHYPTIPAARCLAQFFFFYAFGVTDTLVIAVMALDRYVAICD  
 PLHYALVMNHQRCACLLALS WVVSILHTMLRVGLVPLCWTGDAGGNVNLPHFFCDHRPLLR  
 ASCSDIHSNELAIFFEGLMLGPCALIVLSYVRIGAAILRLPSAAGRRAVSTCGSHLTMVGFL  
 YGTIICVYFQPPFQNSQYQDMVASVMTAITPLANPFVYSLHNKDVKGALCRLLEWVKVDP  
 (SEQ ID NO: 55)  
 45  
 ATGATGAGCTTTGCCCTAATGCTTCACACTCTCCGGTTTTTTTTGCTCCTTGGGTTCTCGAG  
 AGCTAACATCTCCTACACTCTCCTCTTCTCCTGTTCTCCTGGCTATTTACCTGACCACCATAC  
 TGGGGAATGTGACACTGGTGCTGCTCATCTCCTGGGACTCCAGACTGCACTCACCCATGTA  
 TTATCTGCTTCGTGGCCTCTCTGTGATAGACATGGGGCTATCCACAGTTACACTGCCCCAG  
 50 TTGCTGGCCCATTTGGTCTCTCATTACCCAACCATTCCTGCTGCCCCGCTGCTTGGCTCAGTT  
 CTTTTCTTCTATGCATTTGGGGTTACAGATACACTTGTCAATTGCTGTGCTGCTGCTGATC  
 GCTATGTGGCCATCTGTGACCCCTGCACTATGCTTTGGTAATGAATACCAACGGTGTGC  
 CTGCTTACTAGCCTTGAGCTGGGTGGTGTCCATACTGCACACCATGTTGCGTGTGGGACTC  
 GTCCTGCCTCTTTGCTGGACTGGGGATGCTGGGGGCAACGTTAACCTTCCTCACTTCTTTTG  
 55 TGACCACCGGCCACTTCTGCGAGCCTCTTGTCTGACATACATTCTAATGAGCTGGCCATA  
 TTCTTTGAGGGTGGCTTCCTTATGCTGGGCCCCCTGTGCCCTCATTGTACTCTCTTATGTCCG

AATTGGGGCCGCTATTCTACGTTTGCCTTCAGCTGCTGGTCGCCGCCGAGCAGTCTCCACC  
 TGTGGATCCCACCTCACCATGGTTGGTTTCCTCTACGGCACCATCATTGTGTCTACTTCCA  
 GCCTCCCTTCCAGAACTCTCAGTATCAGGACATGGTGGCTTCAGTAATGTATACTGCCATT  
 ACACCTTTGGCCAACCCATTTGTGTATAGCCTCCACAATAAGGATGTCAAGGGTGCCTCT  
 5 GCAGGCTGCTTGAATGGGTGAAGGTAGACCCCTGA (SEQ ID NO: 56)

**AOLFR30 sequences:**

MGFLSPMHPCRPPTQRRMAAGNHSTVTEFILKGLTKRADLQLPLFLFLGIYLVTVGNLGMIT  
 LICLNSQLHTPMYYFLSNLSLMDLCYSSVITPKMLVNFVSEKNII SYAGCMSQLYFFLVFVIAEC  
 10 YMLTVMA YDRYVXXCHPLLYNIIMSHHTCLLLVAVVYAIGLIGSTIETGLMLKLPYCEHLISHY  
 FCDILPLMKLSCSSYDVEMTVFFSAGFNII VTS LTVLVSYTFILSSILGISTTEGRSKAFSTCSSHL  
 AAVGMFYGSTAFMYLKPSTISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKA AVQKTLRGK  
 LF (SEQ ID NO: 57)  
 15 ATGGGGTTCTTGTCTCCCATGCATCCCTGCAGGCCTCCCACCCAGAGGAGAATGGCTGCAG  
 GAAATCACTCTACAGTGACAGAGTTTCTTCAAGGGTTTAACGAAGAGAGCAGACCTCC  
 AGCTCCCCCTCTTCTCCTCTTCTCGGGATCTACTTGGTCACCATCGTGGGGAACCTGGGC  
 ATGATCACTCTAATTTGTCTGAACTCTCAGCTGCACACCCCATGTACTACTTTCTCAGCAA  
 TCTGTCACTCATGGATCTCTGCTACTCCTCCGTCATTACCCCTAAGATGCTGGTGAACCTTG  
 20 TGTCAGAGAAAAACATCATCTCCTACGCAGGGTGCATGTCACAGCTCTACTTCTTCTTGT  
 TTTTGTCAATTGCTGAGTGTTACATGCTGACAGTGATGGCCTACGACCGCTATGTTGNCNTC  
 TGCCACCCTTTGCTTTACAACATCATTATGTCTCATCACACCTGCCTGCTGCTGGTGGCTGT  
 GGTCTACGCCATCGGACTCATTGGCTCCACAATAGAAACTGGCCTCATGTTAAACTGCCC  
 TATTGTGAGCACCTCATCAGTCACTACTTCTGTGACATCCTCCCTCTCATGAAGCTGTCTCTG  
 25 CTCTAGCACCTATGATGTTGAGATGACAGTCTTCTTTTCGGCTGGATTCAACATCATAGTC  
 ACGAGCTTAACAGTTCTTGTCTTACACCTTCATTCTCTCCAGCATCCTCGGCATCAGCAC  
 CACAGAGGGGAGATCCAAAGCCTTCAGCACCTGCAGCTCCCACCTTGACGCCGTGGGAAT  
 GTTCTATGGATCAACTGCATTCTGTACTTAAACCCCTCCACAATCAGTTCCTTGACCCAG  
 GAGAATGTGGCCTCTGTGTTCTACACCACGGTAATCCCCATGTTGAATCCCCTAATCTACA  
 30 GCCTGAGGAACAAGGAAGTAAAGGCTGCCGTGCAGAAAACGCTGAGGGGTAAACTGTTTT  
 GA (SEQ ID NO: 58)

**AOLFR31 sequences:**

MGTGNDTTVVEFTLLGLSEDTTVCAILFLVFLGIYVVTLMGNISIIVLIRSHHLHTPMYIFLCHL  
 35 AFVDIGYSSSVTPVMLMSFLRKETSLPVAGCVAQLCSVVTFGTAECFLLAAMAYDRYVAICSP  
 LLYSTCMSPGVCHLVGMSYLGGCVNAWTFIGCLLRLSFCGPNKVNHHFFCDYSPLKLACSHDF  
 TFEIIPAISGSIIVATVCVIAISYIYILITILKMHSTKGRHKAFSTCTSHLTAVTLFYGTITFIYVMP  
 KSSYSTDQNKVVS VFYTVVIPMLNPLIYSLRNKEIKGALKRELRIKIFS (SEQ ID NO: 59)  
 40 ATGGGGACTGGAAATGACACCACTGTGGTAGAGTTTACTCTTTTGGGGTTATCTGAGGATA  
 CTACAGTTTGTGCTATTTTATTTCTTGTGTTTCTAGGAATTTATGTTGTACCTTAATGGGT  
 AATATCAGCATAATTGTATTGATCAGAAGAAGTCATCATCTTCATACACCCATGTACATTT  
 TCCTCTGCCATTTGGCCTTTGTAGACATTGGGTACTCCTCATCAGTCACACCTGTCATGCTC  
 ATGAGCTTCCTAAGGAAAGAAACCTCTCTCCCTGTTGCTGGTTGTGTGGCCAGCTCTGTT  
 45 CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCTGCTGGCTGCCATGGCCTATGATCGCTA  
 TGTGGCCATCTGCTCACCCCTGCTCTACTCTACCTGCATGTCCCCTGGAGTCTGCATCATCT  
 TAGTGGGCATGTCCTACCTGGGTGGATGTGTGAATGCTTGGACATTCAATTGGCTGCTTATT  
 AAGACTGTCCTTCTGTGGGCCAAATAAAGTCAATCACTTTTCTGTGACTATTCAACCACTTT  
 TGAAGCTTGCTTGTTCCTCATGATTTTACTTTTGAAATAATTCCAGCTATCTCTTCTGGATCT  
 50 ATCATTGTGGCCACTGTGTGTGTCATAGCCATATCCTACATCTATATCCTCATCACCATCCT  
 GAAGATGCACTCCACCAAGGGCCGCCACAAGGCCTTCTCCACCTGCACCTCCCACCTCACT  
 GCAGTCACTCTGTTCTATGGGACCATTACCTTCATTTATGTGATGCCCAAGTCCAGCTACTC  
 AACTGACCAGAACAAAGGTGGTGTCTGTGTTCTACACCGTGGTGATTCCCATGTTGAACCCC  
 CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA  
 55 AAAATATTTTCTTGA (SEQ ID NO: 60)

**AOLFR32 sequences:**

MNSLKDG NHTALTGFILLGLTDDPILRVILFMILSGNLSIIILIRISSQLHHPMYFFLSHLAFADM  
AYSSSVTPNMLVNFLVERNTVSYLGCAIQLGSAFFATVECVLLAAMAYDRFVAICSPLLYSTK  
MSTQVSVQLLLVVYIAGFLIAVSYTTSFYLLFCGPNQVNHFFCDFAPLLELSCSDISVSTVVLFSF  
5 SSGSIHVTVVCVIAVCYIYILITILKMRSTEGHHKAFSTCTSHLTVVTLFYGTITFIYVMPNFSYST  
DQNKVVS VLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNDIT (SEQ ID  
NO: 61)

ATGAATTCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA  
10 CAGATGATCCAATCCTTCGAGTCATCCTCTTCATGATCATCCTATCTGGTAATCTCAGCATA  
ATTATCTTATCAGAATTTCTTCTCAGCTCCATCATCCTATGTATTTCTTTCTGAGCCACTT  
GGCTTTTGCTGACATGGCCTATTCTCTGTGACACCCAACATGCTTGTAACCTTCCTGG  
TGGAGAGAAATACAGTCTCCTACCTTGATGTGCCATCCAGCTTGGTTCAGCGGCTTTCTT  
TGCAACAGTCGAATGCGTCCTTCTGGCTGCCATGGCCTATGACCGCTTTGTGGCAATTTGC  
15 AGTCCACTGCTTTATTCAACCAAAATGTCCACACAAGTCAGTGTCCAGCTACTCTTAGTAG  
TTTACATAGCTGGTTTTCTCATTTGCTGTCTCCTATACTACTTCCTTCTATTTTTTACTCTTCT  
GTGGACCAAAATCAAGTCAATCATTTTTCTGTGATTTTCGCTCCCTTACTTGAACCTCTCCTGT  
TCTGATATCAGTGTCTCCACAGTTGTTCTCTCATTTTCTTCTGGATCCATCATTTGTGGTCAC  
TGTGTGTGTCTAGCCGTCTGCTACATCTATATCCTCATCACCATCCTGAAGATGCGCTCCA  
20 CTGAGGGGCACCACAAGGCCTTCTCCACCTGCACTTCCACCTCACTGTGGTTACCCTGTT  
CTATGGGACCATTACCTTCATTTATGTGATGCCCAATTTTAGCTACTCAACTGACCAGAAC  
AAGGTGGTGTCTGTGTTGTACACAGTGGTGATTCCCATGTTGAACCCCTGATCTACAGCC  
TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTTAGAAAAATACTTTCTC  
ATGATGCTTGTTATTTTAGTAGAACTTCAAATAATGATATTACATAG (SEQ ID NO: 62)

25

**AOLFR34 sequences:**

MLEGVEHLLLLLLLLTDVNSKELQSGNQTSVSHFILVGLHHPPLGAPLFLAFLVIYLLTVSGNG  
LIILTVLVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLGSRIISFGGCVIQLFSFHLGCT  
ECFLYTL MAYDRFLAICKPLHYATIMTHRVCNLSALGTWLG GTIHSLSFQTSFVRLPFCGPNRV  
30 DYIFCDIPAMRLACADTAINELVTFADIGFLALTCFMLILTSYGYIVAAILRIPSADGRRNAFST  
CA AHLTVVIVVYVPCTFIYLRPCSQEPLDGVVAVFYTVITPLLNSIYTLCKEMKAALQRLGG  
HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTTGAGCATCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG  
35 AACTGCAAAGTGGAACCAGACTTCTGTGTCTCACTTCATTTTGGTGGGCCTGCACCACCC  
ACCACAGCTGGGAGCGCCACTCTTCTTAGCTTTCTTGTGATCTATCTCCTCACTGTTTCTG  
GAAATGGGCTCATCATCCTCACTGTCTTAGTGGACATCCGGCTCCATCGTCCCATGTGCTT  
GTTCTGTGTACCTCTCCTTCTTGGACATGACCATTTCTTGTGCTATTGTCCCCAAGATGC  
TGGCTGGCTTTCTCTTGGGTAGTAGGATTATCTCCTTTGGGGGCTGTGTAATCCAATATTT  
40 TCTTTCCATTTCTTGGGCTGTACTGAGTGCTTCTTTACACACTCATGGCTTATGACCGTTT  
CCTTGCCATTTGTAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCTGTAACCTCCC  
TGGCTTAGGCACCTGGCTGGGAGGGACTACCATTCATTTTCCAAACAAGTTTTGTATT  
CCGGCTGCCCTTCTGTGGCCCAATCGGGTGCAGTACATCTTCTGTGACATTCTGCCATGC  
TGCGTCTAGCCTGCGCCGATACGGCCATCAACGAGCTGGTCACCTTTGCAGACATTGGCTT  
45 CCTGGCCCTCACCTGCTTCATGCTCATCCTCACTTCCTATGGCTATATTGTAGCTGCCATCC  
TGCGAATTCGTCAGCAGATGGGCGCCGAATGCCTTCTCCACTTGTGCTGCCACCTCAC  
TGTTGTCAATTGTTTACTATGTGCCCTGCACCTTCATTTACCTGCGGCCTTGTTACAGGAGC  
CCCTGGATGGGGTGGTAGCTGTCTTTACACTGTCATCACTCCCTTGCTTAACCTCCATCATC  
TACACACTGTGCAACAAAGAAATGAAGGCAGCATTACAGAGGCTAGGGGGGCCACAAGGAA  
50 GTGCAGCCTCACTGA (SEQ ID NO: 64)

**AOLFR35 sequences:**

MEPLNRTEVSEFFLKGFSGYPALHLLFPLCSAMYLVTLGNTAIMAVSVLDIHLHTPVYFFLG  
NLSTLDICYTPTFVPLMLVHLLSSRK TISFAVCAIQMCLSLSTGSTECLLLAITAYDRYLAICQPL  
55 RYHVLMSHRLCVLLMGAAWVLCLLKSVTEMVISMRLPFCGHHVVSHTCKILAVLKLACGNT  
SVSEDFLLAGSILLPVPLAFICLSYLLILATILRVPSAARCKAFSTCLAHLAVVLLFYGTIIFMY

LKPKSKEAHISDEVFTVLYAMVTTMLNPTIYSLRNKEVKEAARKVWGRSRASR (SEQ ID NO: 65)

5 ATGGAGCCGCTCAACAGAACAGAGGTGTCCGAGTTCTTTCTGAAAGGATTTTCTGGCTACC  
CAGCCCTGGAGCATCTGCTCTTCCCTCTGTGCTCAGCCATGTACCTGGTGACCCTCCTGGG  
GAACACAGCCATCATGGCGGTGAGCGTGCTAGATATCCACCTGCACACGCCCGTGTACTTC  
TTCTGGGCAACCTCTCTACCCTGGACATCTGCTACACGCCACCTTTGTGCCTCTGATGCT  
GGTCCACCTCCTGTATCCCGGAAGACCATCTCCTTTGCTGTCTGTGCCATCCAGATGTGTC  
10 TGAGCCTGTCCACGGGCTCCACGAGTGCCTGCTACTGGCCATCACGGCCTATGACCGCTA  
CCTGGCCATCTGCCAGCCACTCAGGTACCACGTGCTCATGAGCCACCGGCTCTGCGTGCTG  
CTGATGGGAGCTGCCTGGGTCCTCTGCCTCCTCAAGTCGGTGACTGAGATGGTCATCTCCA  
TGAGGCTGCCCTTCTGTGGCCACCACGTGGTCAGTCACTTCACCTGCAAGATCCTGGCAGT  
GCTGAAGCTGGCATGCGGCAACACGTGGTCAGCGAAGACTTCCTGCTGGCGGGCTCCAT  
15 CCTGCTGCTGCTGTACCCCTGGCATTATCTGCCTGTCTACTTGCTCATCCTGGCCACCA  
TCCTGAGGGTGCCCTCGGCCGCCAGGTGCTGCAAAGCCTTCTCCACCTGCTTGGCACACCT  
GGCTGTAGTGCTGCTTTTCTACGGCACCATCATCTTCATGTACTTGAAGCCCAAGAGTAAG  
GAAGCCACATCTCTGATGAGGTCTTCACAGTCTCTATGCCATGGTCACGACCATGCTGA  
ACCCACCATCTACAGCCTGAGGAACAAGGAGGTGAAGGAGGCCGCCAGGAAGGTGTGGG  
GCAGGAGTCGGGCCTCCAGGTGA (SEQ ID NO: 66)

20

**AOLFR36 sequences:**

MYLVTVLRLNLLSILAVSSDSHPHTPMYFFLSNLCWADIGFTLATVPKMIVDMGSHSKVISYGG  
CLTQMSFLVLFACIVDMFLTMAYDCFVAICRPLHYPVIVNPHLCVFFVLVSFFLSLLDSQLHS  
WIVLQFTFFKNVEISNFVCEPSQLKLASYDSVINSIFIYFDNTMFGLPISGILLSYYKIVPSILRIS  
25 SSDGKYKAFSACGCHLAVVCLFYGTGIGVYLTSAPPLRNGMVASVMYAVVTPMLNPFYIS  
LRNRDIQSALWRVCNKTVESHDLFHPFSCVVEKGQPHSIPTSANPAP (SEQ ID NO: 67)

30 ATGTATCTGGTACGGTGCTGAGGAACCTGCTCAGCATCCTGGCTGTCAGCTCTGACTCCC  
ACCCCCACACACCCATGTACTTCTTCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC  
TTGGCCACGGTTCCCAAAATGATTGTGGACATGGGGTCGCATAGCAAAGTCATCTCTTATG  
GGGGCTGCCTGACACAGATGTCTTTCTTGGTACTTTTTGCATGTATAGTAGACATGTTCT  
GACTGTGATGGCTTATGACTGCTTTGTAGCCATCTGTCGCCCTCTGCACTACCCAGTCATC  
GTGAATCCTCACCTCTGTGTCTTCTTCGTTTTGGTGTCCTTTTTCTTAGCCTGTTGGATTCC  
CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAAATCTCTAATT  
35 TTGTCTGTGAGCCATCTCAACTTCTCAAGCTTGCCCTCTTATGACAGCGTCATCAATAGCATA  
TTCATATATTTTGATAATACTATGTTTGGTTTTCTTCCCATTTTCAGGGATCCTTTTGTCTTAC  
TATAAAATTGTCCCTCCATTCTAAGGATTCATCATCAGATGGGAAGTACAAAGCCTTCT  
CAGCCTGTGGCTGTCACCTGGCAGTTGTTTGCTTATTTATGGAACAGGCATTGGCGTGTA  
CCTGACTTCAGCTGTGGCACCACCCCTCAGGAATGGTATGGTGGCGTCAGTGATGTACGCT  
40 GTGGTCACCCCATGCTGAACCTTTTCATCTACAGCCTGAGAAACAGGGACATTCAAAGTG  
CCCTGTGGAGGGTGTGCAACAAACAGTCGAATCTCATGATCTGTTCCATCCTTTTTCTTG  
TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCCTTAG  
(SEQ ID NO: 68)

45 **AOLFR37 sequences:**

MEKANETSPVMGFVLLRLSAHPELEKTFVLLILMYLVILLGNGVLILVTILDSRLHTPMYFFLG  
NLSFLDICFTTSSVPLVLDSFLTPQETISFSACAVQMAISFAMAGTECLLSMMAFDRYVAICNP  
LRYSVIMSKAAYMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS  
INVISMEVTNVIFLGVPVLFISFSYVFIITILRIPSAEGRKKVFSTCSAHLTVVIVFYGTLFFMYG  
50 KPKSKDSMGADKEDLSKLIPLFYGVVTPMLNPIIYSLRNKDVKA AVRLLLRPKGFTQ (SEQ ID  
NO: 69)

55 ATGGAAAAAGCCAATGAGACCTCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCCC  
ACCCAGAGCTGGAAAAGACATTCTTCGTGCTCATCCTGCTGATGTACCTCGTGATCCTGCT  
GGGCAATGGGGTCTCATCCTGGTGACCATCCTTGACTCCCGCTGCACACGCCCATGTAC  
TTCTTCTAGGGAACCTCTCCTTCTGGACATCTGCTTCACTACCTCCTCAGTCCCACTGGT

CCTGGACAGCTTTTTGACTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG  
 GCACTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTGATC  
 GCTATGTGGCCATCTGCAACCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCCTACAT  
 GCCCATGGCTGCCAGCTCCTGGGCTATTGGTGGTGTGCTGCTTCCGTGGTACACACATCCTTG  
 5 GCAATTCAGCTGCCCTTCTGTGGAGACAATGTCAACCACTTCACCTGTGAGATTCTGG  
 CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA  
 TGTGATCTTCCTAGGAGTCCCGTTCTGTTTCATCTCTTTCTCCTATGTCTTCATCATACCA  
 CCATCCTGAGGATCCCCCTCAGCTGAGGGGAGGAAAAAGGTCTTCTCCACCTGCTCTGCCCA  
 CCTCACCGTGGTGATCGTCTTCTACGGGACCTTATTCTTCATGTATGGGAAGCCTAAGTCT  
 10 AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAAACTCATCCCCCTTTTCTATG  
 GGGTGGTGACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG  
 CTGCTGTGAGGAGACTGCTGAGACCAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)

**AOLFR38 sequences:**

15 MYLVTVLRLNLLILAVSSDSLHTPMCFFLSNLCWADIGFTSAMVPMIVDMQSHSRVISYAGC  
 LTQMSFFVLFIACIEDMLLTVMAYDRFVAICHPLHYPVIMNPHLGVELVLVSFFLSLLDSQLHSW  
 IVLQFTFFKNVEISNFVCDPSQLNLACSDSVINSIFIYLD SIMFGFLPISGILLSYANNVPSILRISS  
 SDRKSKAFSTCGSHLAVVCLFYGTGIGVYLTSAVSPPRNGVVASVMYAVVTPMLNPFYSLR  
 NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)

20 ATGTACCTGGTCACGGTGCTGAGGAACCTGCTCATCATCCTGGCTGTGAGCTCTGACTCCC  
 ACCTCCACACCCCCATGTGCTTCTCCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC  
 TCGGCCATGGTTCCTCCCAAGATGATTGTGGACATGCAGTCGCATAGCAGAGTCATCTCTTATG  
 CGGGCTGCCTGACACAGATGTCTTTCTTTGTCCCTTTTTCATGTATAGAAGACATGCTCCTG  
 25 ACAGTGATGGCCTATGACCGATTTGTGGCCATCTGTCACCCCTGCACTACCCAGTCATCA  
 TGAATCCTCACCTTGGTGTCTTCTTAGTTTTGGTGTCTTTTCTCAGCCTGTTGGATTCC  
 CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAATCTCCAATT  
 TTGTCTGTGACCCATCTCAACTTCTCAACCTTGCCTGTTCTGACAGTGTGATCAATAGCATA  
 TTCATATATTTAGATAGTATTATGTTTGGTTTTCTTCCCATTTCAGGGATCCTTTTGTCTTAC  
 30 GCTAACAAATGTCCCTCCATTCTAAGAATTCATCATCAGATAGGAAGTCTAAAGCCTTCT  
 CCACCTGTGGCTCTCACCTGGCAGTTGTTTGCTTATTTTATGGAACAGGCATTGGCGTGTA  
 CCTGACTTCAGCTGTGTCACCAACCCCCCAGGAATGGTGTGGTGGCATCAGTGATGTACGCT  
 GTGGTCACCCCATGCTGAACCCCTTTCATCTACAGCCTGAGAAATAGGGACATTCAAAGTG  
 CCCTGTGGAGGCTGCGCAGCAGAACAGTCGAATCTCATGATCTGTTATCTCAAGATCTGCT  
 35 CCATCCTTTTCTTGTGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)

**AOLFR39 sequences:**

40 MGVDKNHSTVTEFLLSGLTEQAEQLPLFCLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS  
 LSFLDFCYSSVITPKMLSGLCRDRSISYSGCMIQLFFFCVCVISECYMLAAMACDRYVAICSP  
 LYRVIMSPRVCSLLVAAVFSVGFTDAVIHGGCILRLSFCGSNIIKHVFCDIVPLIKLSCSSSTYIDEL  
 LIFVIGGFNMVATSLTIIISYAFILTSILRIHKKGRCKAFSTCSSHLTAVLMFYGSLMSMYLKPAS  
 SSSLTQEKVSSVFYTTVILMLNPLIYSLRNNEVRNALMKLLRRKISLSPG (SEQ ID NO: 73)

45 ATGGGTGTAAAAAACCATTCACAGTGACTGAGTTTCTTCTTTCAGGATTAACCTGAACAAG  
 CAGAGCTTCAGCTGCCCCCTTCTGCCTCTTCTTAGGAATTTACACAGTTACTGTGGTGGG  
 AAACCTCAGCATGATCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCATGTACTAT  
 TTCCTGAGTAGTTTGTCTTTTTTAGATTTCTGCTATTCTTCTGTCATTACCCCTAAAATGCT  
 ATCAGGGTTTTTATGCAGAGATAGATCCATCTCCTATTCTGGATGCATGATTCAGCTGTTTT  
 TTTTCTGTGTTTGTGTTATTTCTGAATGTACATGCTGGCAGCCATGGCCTGCGATCGTAC  
 50 GTGGCCATCTGCAGCCCACTGCTCTACAGGTGTCATCATGTCCCCCTAGGGTCTGTTCTCTGC  
 TGGTGGCTGTGCTTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGTTGTATACT  
 CAGTTTGTCTTTCTGTGGATCAAACATCATTAAACATTATTTCTGTGACATTGTCCCTCTTA  
 TTAAACTCTCCTGCTCCAGCACTTATATTGATGAGCTTTTGATTTTTGTGATTGGTGGATTT  
 AACATGGTGGCCACAAGCCTAACAAATCATTATTTTCATATGCTTTTATCCTCACCAGCATCCT  
 55 GCGCATCCACTCTAAAAAGGGCAGGTGCAAAGCGTTTAGCACCTGTAGCTCCACCTGACA  
 GCTGTTCTTATGTTTTATGGGTCTCTGATGTCCATGTATCTCAAACCTGCTTCTAGCAGTTC

ACTCACCCAGGAGAAAGTATCCTCAGTATTTTATACCACTGTGATTCTCATGTTGAATCCC  
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAACTTTTAAGAAGA  
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

5 **AOLFR40 sequences:**

MSNATLLTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS  
FIDMWFSTVTVPKMLMTLVSPSGRTISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL  
RYTNMMTGRSCALLATGTWLSGSLHSAVQTLTFHLPYCGPNQIQHYFCDAPPILKLACADTS  
ANEMVIFVNIGLVASGCFVLIVLSYVSIVCSILRIRTSEGRHRAFQTCASHCIVVLCFFGPGLFIYL  
10 RPSRDALHGVAVFYTTLTPLFNPVYTLRNKEVKKALLKLKNGSVFAQGE (SEQ ID NO:  
75)

ATGTCCAACGCCACCCTACTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC  
TGGACGCCCCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT  
15 CCTCATCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCCTCA  
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCAAAATGCTGATGAC  
CTTGGTGTCCCCAAGCGGCAGGACTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT  
TCCACTTCCTGGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCCTATGATCGCTACCT  
GGCCATCAGTTACCCGCTCAGGTACACCAACATGATGACTGGGCGCTCGTGTGCCCTCCTG  
20 GCCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCC  
ATTTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCATCCT  
GAAACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGAATATTGGGCTA  
GTGGCTCGGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCT  
GCGGATCCGCACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC  
25 GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCATTTACCTGAGGCCAGGCTCCAGGGACGC  
CTTGATGGGGTTGTGGCCGTTTTCTACACCACGCTGACTCCTCTTTTCAACCCTGTTGTGT  
ACACCCTGAGAAACAAGGAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTCAAGTAT  
TTGCTCAGGGTGAATAG (SEQ ID NO: 76)

30 **AOLFR41 sequences:**

MNPENWTQVTSFVLGFPSSHLIQFLVFLGLMVTYIVTATGKLLIIVLSWIDQRLHIQMYFFLRN  
FSFLELLLVTVVVPKMLVVILTGHTISFVSCIIQSYLYFFLGTDFLLAVMSLDRLAICRPLR  
YETLMNGHVCSQLVLASWLAGFLWVLCPTVLMASLPFCGPNIDHFFRDSWPLRLSCGDTH  
LLKLVAFMLSTLVLLGSLALTSVSYACILATVLRAPTAERKAFSTCASHLTVVVIIYGSSIFLY  
35 IRMSEAQSKLLNKGASVLSCHITPLNPFIFTLRNDKVQQALREALGWPRLTAVMKLRVTSQRK  
(SEQ ID NO: 77)

ATGAACCCTGAAAACCTGGACTCAGGTAACAAGCTTTGTCCTTCTGGGTTTCCCCAGTAGCC  
ACCTCATACAGTTCCTGGTGTTCTGGGGTTAATGGTGACCTACATTGTAACAGCCACAGG  
40 CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCTGCACATACAGATGTACTTC  
TTCCTGCGGAATTTCTCCTTCCTGGAGCTGTTGCTGGTAACTGTTGTGGTTCCCAAGATGCT  
TGTCGTCATCCTCACGGGGGATCACACCATCTCATTTGTCAGCTGCATCATCCAGTCCTACC  
TCTACTTCTTTCTAGGCACCACTGACTTCTCCTCTTGGCCGTCATGTCTCTGGATCGTTAC  
CTGGCAATCTGCCGACCACTCCGCTATGAGACCCTGATGAATGGCCATGTCTGTTCCCAAC  
45 TAGTGCTGGCCTCCTGGCTAGCTGGATTCTCTGGGTCTTTGCCCCACTGTCCTCATGGCC  
AGCCTGCCTTTCTGTGGCCCCAATGGTATTGACCACTTCTTTCGTGACAGTTGGCCCTTGCT  
CAGGCTTTCTTGTTGGGGACACCCACCTGCTGAAACTGGTGGCTTTTCATGCTCTCTACGTTG  
GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCTATGCTGCATTCTTGCCACTGTTCT  
CAGGGCCCCCTACAGCTGCTGAGCGAAGGAAAGCGTTTTCCACTTGCGCCTCGCATCTTACA  
50 GTGGTGGTCATCATCTATGGCAGTTCATCTTTCTACATTCTGATGTGAGAGGCTCAGTC  
CAAAGTGTCAACAAGGTGCCTCCGCTCTGAGCTGCATCATCACACCCCTCTTGAACCCA  
TTCATCTTCACTCTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTGGGGTGGC  
CCAGGCTCACTGCTGTGATGAAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO:  
78)

55



**AOLFR42 sequences:**

MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSAVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL  
GNLSFLDFCYSSITAPRMLVDLLSGNPTISFGGCLTQLFFHFIGGIKIFLLTVMAYDRYIAISQPL  
HYTLIMNQTVCALLMAASWVGFIHSIVQIALTIQLPFCGPKLDNFYCDVPQLIKLACTDTFV  
5 LELLMVSNNGLVTLMCFLVLLGSYTALLVMLRSHSREGRSKALSTCASHIAVVTLIFVPCIYVY  
TRPFRTPMDKAVSVLYTIVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGPLEHRPLH  
(SEQ ID NO: 79)

10 ATGAATCCAGCAAATCATTCCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT  
GGGAGCTTCGGTTTGTCTTCTCACTGTTTTCTCTGCTGTGTATTTTATGACTGTAGTGGGA  
AACCTTCTTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCATGTATTTTCT  
CTTGGGCAATCTTTCTTCTGACTTTTGTCTACTCTTCCATCACAGCACCTAGGATGCTGG  
TTGACTTGCTCTCAGGCAACCCTACCATTTCCCTTGGTGGATGCCTGACTCAACTCTTCTTC  
15 TTCCACTTCATTGGAGGCATCAAGATCTTCTGCTGACTGTCATGGCGTATGACCGCTACA  
TTGCCATTTCCCAGCCCCTGCACTACACGCTCATTATGAATCAGACTGTCTGTGCACTCCTT  
ATGGCAGCCTCCTGGGTGGGGGGCTTATCCACTCCATAGTACAGATTGCATTGACTATCC  
AGCTGCCATTCTGTGGGCCTGACAAGCTGGACAACCTTTTATTGTGATGTGCCTCAGCTGAT  
CAAATTGGCCTGCACAGATACCTTTGTCTTAGAGCTTTTAATGGTGTCTAACAATGGCCTG  
20 GTGACCCTGATGTGTTTTCTGGTGCTTCTGGGATCGTACACAGCACTGCTAGTCATGCTCC  
GAAGCCACTCACGGGAGGGCCGAGCAAGGCCCTGTCTACCTGTGCCTCTCACATTGCTGT  
GGTGACCTTAATCTTTGTGCCTTGCATCTACGTCTATACAAGGCCTTTTCGGACATTCCCCA  
TGGACAAGGCCGTCTCTGTGCTATACACAATTGTCAACCCCATGCTGAATCCTGCCATCTA  
TACCCTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG  
25 ACCCTATTGGTCCCCTGGAGCACAGACCCTTACATTAG (SEQ ID NO: 80)

**AOLFR43 sequences:**

MQKPQLLVPIIATSNGNLVHAAFYLLVGIPGLGPTIHFWLAFPLCFMYALATLGNLTIVLIIRVE  
RRLHEPMYLFLAMLSTIDLVLSSITMPKMASLFLMGIQEIEFNICLAQMFLIHALSAVESAVLLA  
MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFPLPFILKWSYQCQHTVTHSFCLHQ  
30 DIMKLSCTDRVNVVYGLFIILSVMGVDSLFIGFSYILILWAVLELSSRRAALKAFNTCISHLCAV  
LVFYVPLIGLSVVHRLGGPTSLHHVVMANTYLLPVPVNPLVYGAKTKEICSRVLCMFSSQGGK  
(SEQ ID NO: 81)

35 ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG  
CAGCATACTTCCTTTTGGTGGGTATCCCTGGCCTGGGGCCTACCATACACTTTTGGCTGGCT  
TTCCCACTGTGTTTTATGTATGCCTTGCCACCCTGGGTAACCTGACCATTGTCTCATCAT  
TCGTGTGGAGAGGCGACTGCATGAGCCCATGTACCTCTTCCCTGGCCATGCTTTCCACTATT  
GACCTAGTCCTCTCCTCTATCACCATGCCAAGATGGCCAGTCTTTTCTGATGGGCATCCA  
GGAGATCGAGTTCAACATTTGCCTGGCCCAGATGTTCCCTATCCATGCTCTGTGAGCCGTG  
40 GAGTCAGCTGTCTGCTGGCCATGGCTTTTGACCGCTTTGTGGCCATTTGCCACCCATTGC  
GCCATGCTTCTGTGCTGACAGGGTGTACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG  
GGGTTTGTATTCTTCTTCCCACTGCCCTTCATCCTCAAGTGGTTGTCTACTGCCAAACAC  
ATACTGTACACACTCCTTCTGTCTGCACCAAGATATTATGAAGCTGTCTGTACTGACAC  
CAGGGTCAATGTGGTTTATGGACTCTTCATCATCCTCTCAGTCATGGGTGTGGACTCTCTCT  
45 TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTTGGAGCTGTCTCTCGGAGGGCA  
GCACTCAAGGCTTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTTCTATGTACC  
CCTCATTTGGCTCTCGGTGGTGCATAGGCTGGGTGGTCCACCTCCCTCCTCCATGTGGTT  
ATGGCTAATACCTACTTGCTGCTACCACCTGTAGTCAACCCCTTGTCTATGGAGCCAAGA  
50 CCAAAGAGATCTGTTCAAGGGTCTCTGTATGTTCTCACAAGGTGGCAAGTGA (SEQ ID  
NO: 82)

**AOLFR44 sequences:**

MSSCNFTHATFVLIGIPGLEKAHFWVGFPLLSMYVVMFNGNCIVVFIVRTERSLHAPMYLFLC  
MLAAIDLALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPL  
55 RHAAVLNNTVTAQIGIVAVVRGSLFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYADTLF  
NVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAIFYVPLIGLS

VVHFRGNSLHPVVRVVMGDIYLLPPVINPIIYGAKTKQIRTRVLAMFKISCDKDLQAVGGK  
(SEQ ID NO: 83)

5 ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA  
AAGCCCATTCTGGGTGGCTTCCCCCTCCTTTCCATGTATGTAGTGGCAATGTTTGAAAC  
TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTC  
TCTGCATGCTTGACGCCATTGACCTGGCCTTATCCACATCCACCATGCCTAAGATCCTTGCC  
CTTTTCTGGTTTGATTCCCGAGAGATTAGCTTTGAGGCCTGTCTTACCCAGATGTTCTTTAT  
10 TCATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCCATGGCCTTTGACCGTTATGTGG  
CCATCTGCCACCCACTGCGCCATGCTGCAGTGTCAACAATACAGTAACAGCCCAGATTGG  
CATCGTGGCTGTGGTCCGCGGATCCCTCTTTTTTTTCCCACTGCCTCTGCTGATCAAGCGGC  
TGGCCTTCTGCCACTCCAATGTCCCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAA  
GTTGGCCTATGCAGACACTTTGCCCAATGTGGTATATGGTCTTACTGCCATTCTGCTGGTC  
ATGGGCGTGGACGTAATGTTTCATCTCCTTGCTCTATTTTCTGATAATACGAACGGTTCTGC  
15 AACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGTGCACACATTGGTGT  
GGTACTCGCCTTCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCGCTTTGGAAACAGC  
CTTCATCCCATTGTGCGTGTGTGCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCATCAA  
TCCCATCATCTATGGTGCCAAAACCAAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG  
ATCAGCTGTGACAAGGACTTGCAAGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

20

**AOLFR45 sequences:**

MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIIQADAALHEPMYLFLA  
MLATIDLVLSSSTTLPKMLAIFWFRDQENFACLVQMFFLHFSFIMESAVLLAMAFDRYVAICKP  
LHYTTVLTGSLITKIGMAAVARAVTLMPLPFLRRFHYCRGPVIAHCYCEHMAVVRLACGDT  
25 SFNNIYGIAMFVSVDLLFVLSYVFILQAVLQLASQEARYKAFGTCVSHIGAILSTYTPVVIS  
SVMHRVARHAAPRVHILLAIFYLLFPPMVNPIIYGVKTKQIREYVLSLFQRKNM (SEQ ID NO:  
85)

30 TGGAAACAAGAGGTAATCTTTGCAGGTGGGATAGCACAGGTTGAACTCTAATCATATATA  
CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTTCCA  
GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTTGTGGTAGGAAT  
TCCTGGTTTGGAAACACCTGCATGCCTGGATCTCCATCCCCTTCTGCTTTGCTTATACTCTGG  
CCCTGCTAGGCAACTGTACCCTTCTCTTATTATCCAGGCTGATGCAGCCCTCCATGAACCC  
ATGTACCTCTTTCTGGCCATGTTGGCAACCATTGACTTGGTTCTTTCTTCTACAACGCTGCC  
35 CAAAATGCTTGCCATATTCTGGTTCAGGGATCAGGAGATCAACTTCTTTGCCTGTCTGGTC  
CAGATGTTCTTCCCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGTCTGCTGGCCATGGCCTT  
TGACCGCTATGTGGCCATCTGCAAGCCATTGCACTACACGACGGTCCTGACTGGGTCCCTC  
ATCACCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCT  
TCCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCCATGTACTGTGAACA  
40 CATGGCTGTGGTAAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATGTGT  
GTGGCCATGTTTAGTGTGGTGTGGACCTGCTCTTTGTTATCCTGTCTTATGTCTTCATCCT  
TCAGGCAGTTCTCCAGCTGCCTCTCAGGAGGCCCGCTACAAAGCATTGGGACATGTGTG  
TCTCACATAGGTGCCATCCTGTCCACCTACACTCCAGTAGTCATCTCTTCAGTCATGCACCG  
TGTAGCCCGCCATGCTGCCCCCTCGTGTCCACATACTCCTTGCTATTTTCTATCTCCTTTCC  
45 CACCCATGGTCAATCCTATCATATATGGAGTCAAGACCAAGCAGATTCGTGAGTATGTGCT  
CAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTTTTTATCCCACTTGCCA  
AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAAATTGCAGAGT  
ATCTTTGACAATTCTCTAGTATGATAAGGAAAAATGAGGTTTCATTCCTCACAGATCTACGA  
GTCAAGTCAAACAGGAGTGCACCTATAGTCTGGTCTGATAGTAGAGGTTTGACCTTCCCA  
50 TTGTCATAGACTCATCATGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAAATCTG  
GGTGAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCCAAACAGCTGAGTC (SEQ ID  
NO: 86)

**AOLFR46 sequences:**

55 MNIKHCGWHMIHTWLNIREDDDSDFKNFIGIQGLSGNPHSTTSRMYFLCFCTSLLGFKVHWV  
SRLIXKLYMASPNNDSTAPVSEFLICFPNFQSWQHWLSLPLSLLFLAMGANTLLITIQLAS

LHQPLYLLSLLSLLDIVLCLTVIPKVLAIWFDFLRISFPACFLQMFIMNSFLTMESCTFMVMA  
YDRYVAICHPLRPSIITDQFVARAVFVIARNAFVSLPVPMLSARLRYCAGNIKNCICSNLSVS  
KLSCDDITFNQLYQFVAGWTLGSDLILVISYSFILKVVLRKAEGAVAKALSTCGSHFILILFFS  
TVLLVLVITNLARKRIPDPVILLNLHLLIPPALNPVYGVRTKEIKQGIQNLLKRL (SEQ ID NO:

5 87)

ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT  
GATGACAGTGATTTTAAAACTTTATTGGACAGATACAGGGCCTCAGTGGAAACCCACACT  
CTACTACGTCTAGAATGTACTTTTTATGTTTCTGTACTTCTCTACTAGGTTTAAAGGTACAC  
10 TGGGTCTCCAGATTGATCANGAACTTTACATGGCATCTCCCAACAATGACTCCACTGCCC  
CAGTCTCTGAATTCCTCCTCATCTGCTTCCCCAACTTCCAGAGCTGGCAGCACTGGTTGTCT  
CTGCCCCCTCAGCCTTCTCTTCTCCTGGCCATGGGAGCTAACACCACCCTCCTGATCACCAT  
CCAGCTGGAGGCCTCTCTGCACCAGCCCCGTGACTACCTGCTCAGCCTCCTCTCCCTGCTGG  
ACATCGTGCTCTGCCTCACCCTCATCCCCAAGGTCCTGGCCATCTTCTGGTTTGACCTCAGG  
15 TCGATCAGCTTCCCAGCCTGCTTCTCCAGATGTTTCATCATGAACAGTTTTTTGACCATGGA  
GTCCTGCACGTTTCATGGTCATGGCCTATGACCGTTATGTGGCCATCTGCCATCCATTGAGA  
TACCCGTCTATCATCACTGACCAGTTTGTGGCTAGGGCCGTGGTCTTTGTTATAGCCCGGA  
ATGCCTTTGTTTCTCTTCTGTTCCCATGCTTTCTGCCAGGCTCAGATACTGTGCAGGAAAC  
ATAATCAAGAACTGCATCTGCAGTAACCTGTCTGTGTCCAACTCTCTTGATGACATCA  
20 CTTTCAATCAGCTCTACCAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTTATCCTT  
ATTGTTATCTCCTATTCTTTATATGAAAGTTGTGCTTAGGATCAAGGCCGAGGGTGCTGT  
GGCCAAGGCCTTGAGCACGTGTGGTTCCCACTTCATCCTCATCCTCTTCTTACGACAGTCC  
TGCTGGTTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCTCCAGATGTCCCCATCCT  
GCTCAACATCCTGCACCACCTCATTCCCCCAGCTCTGAACCCCATTTGTTTATGGTGTGAGA  
25 ACCAAGGAGATCAAGCAGGGAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

**AOLFR47 sequences:**

MSASNITLTHPTAFLLVGIPGLEHLHIWISIPCLAYTLALLGNCTLLLIQADAALHEPMYLFLA  
MLAAIDLVLSSALPKMLAIFWFRDREINFFACLAQMFFLHFSFIMESAVLLAMAFDRYVAICK  
30 PLHYTKVLTGSLITKIGMAAVARAVTLMTPLPFLRCHFHYCRGPVIAHCYCEHMAVVRLACGD  
TSFNNIYGIAVAMFIVVLDLLVILSYIFILQAVLLASQEARYKAFGTCVSHIGAILAFYTTVVIS  
SVMHRVARHAAPHVHILLANFYLLFPPMVNPVYGVKTKQIRESILGVFPRKDM (SEQ ID NO:

89)

ATGTCAGCCTCCAATATCACCTTAACACATCCAAGTGCCTTCTTGTGGTGGGGATTCCAG  
GCCTGGAACACCTGCACATCTGGATCTCCATCCCTTTCTGCTTAGCATATACACTGGCCCTG  
CTTGGAACCTGCACTCTCCTTCTCATCATCCAGGCTGATGCAGCCCTCCATGAACCCATGT  
ACCTCTTTCTGGCCATGTGTGGCAGCCATCGACCTGGTCCTTCTCCTCAGCACTGCCAAA  
ATGCTTGCCATATTCTGGTTCAGGGATCGGGAGATAAACTTCTTTGCCTGTCTGGCCAGA  
40 TGTCTTCTCCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTTTGAC  
CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGTCCTGACTGGGTCCCTCATCA  
CCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCTTCT  
GCTGAGATGTTTCCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGAACACATG  
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTGG  
45 CCATGTTTATTGTGGTGTGGACCTGCTCCTTGTATCCTGTCTTATATCTTATTCTTCAG  
GCAGTTCTACTGCTTGCCTCTCAGGAGGCCCGCTACAAGGCATTTGGGACATGTGTCTCTC  
ATATAGGTGCCATCTTAGCCTTCTACACAAGTGTGGTCATCTCTTCAGTCATGCACCGTGTA  
GCCCCGCATGCTGCCCTCATGTCCACATCCTCCTTGCCAATTTCTATCTGCTCTTCCACC  
CATGGTCAATCCCATAATCTATGGTGTCAAGACCAAGCAATCCGTGAGAGCATCTTGGGA  
50 GTATCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

**AOLFR48 sequences:**

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTHIYIVRTEHSLHEPMYIFL  
CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFIAHSLSGMESTVLLAMAFDRYVAICH  
55 PLRHATVLTLPVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHQDVMKLACDDI  
RVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTREAAQAKAFGTCVSHVCAVFIFYVPFIGLSM

VHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVATHASEP (SEQ ID NO: 91)

5 ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC  
CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACCTTATTGCT  
GTGCTAGGTAACCTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCA  
TGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCCC  
AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGCTACA  
GATGTTTGGCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCTTTT  
10 GACCGCTATGTGGCCATCTGTACCCACTGCGCCATGCCACAGTACTTACGTTGCCTCGTG  
TCACCAAAATGGTGTGGCTGCTGTGGTGGGGGGGCTGCACTGATGGCACCCCTTCCTGT  
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCCTACACC  
AAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCCTTATCGT  
CATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGCTTATTCTTA  
15 AGACTGTGTTGGGCTTGACACGTGAAGCCAGGCCAAGGCATTGGCCTTGCCTCTCTCA  
TGTGTGTGCTGTGTTTCATATTCTATGTACCTTTCATTGGATTGTCCATGGTGCATCGCTTGA  
GCAAGCGGCGTGACTCTCCGCTGCCCCGTCATCTTGCCCAATATCTATCTGCTGGTTCTCCTCT  
GTGCTCAACCCCAATTGTCTATGGAGTGAAGACAAAGGAGATTCGACAGCGCATCCTTCGA  
CTTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

20

**AOLFR49 sequences:**

MLTFHNVCSVPSSFVLTGIPGLES LHVWLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF  
LCMLAAIDLVLSTSTIPKLLGIFWFGACDIGLDACLGQMFLIHC FATVESGIFLAMAFDRYVAIC  
NPLRHSMVLTYTVVGR LGLVSLLRGVLYIGPLPLMIRLRLPLYKTHVISHSYCEHMAVVALTC  
25 GDSRVNNVYGLSIGFLVLILDSVAIAASYVMIFRAVMGLATPEARLKT LGTCASHLCAILIFYVP  
IAVSSLIHRFGQCVPPPVTLLANFYLLIPILNPIVYAVRTKQIRESLLQIPRIEMKIR (SEQ ID  
NO: 93)

30 ATGCTCACTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG  
GCTGGAGTCCCTACACGTCTGGCTCTCCATCCCCTTTGGCTCCATGTACCTGGTGGCTGTG  
GTGGGGAATGTGACCATCCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACCAGCCCATG  
TACTTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTTCTGTCTACTTCCACTATACCCAA  
ACTTCTGGGAATCTTCTGGTTTCGGTGCTTGTGACATTGGCCTGGACGCCTGCTTGGGCCAA  
ATGTTCCCTATCCACTGCTTTGCCACTGTTGAGTCAGGCATCTTCCTTGCCATGGCTTTTGA  
35 TCGCTACGTGGCCATCTGCAACCCACTACGTCATAGCATGGTGCTCACTTATACAGTGGTG  
GGTCGTTTGGGGCTTGTCTCTCCTCCGGGGTGTCTCTACATTGGACCTCTGCCTCTGAT  
GATCCGCCTGCGGCTGCCCCTTTATAAAACCCATGTTATCTCCCACTCCTACTGTGAGCAC  
ATGGCTGTAGTTGCCTTGACATGTGGCGACAGCGGTCAATAATGTCTATGGGCTGAGC  
ATCGGCTTTCTGGTGTGATCCTGGACTCAGTGCGTATTGCTGCATCCTATGTGATGATTTT  
40 CAGGGCCGTGATGGGGTAGCCACTCCTGAGGCTAGGCTTAAACCCCTGGGGACATGCGC  
TTCTCACCTCTGTGCCATCCTGATCTTTATGTTCCCATTGCTGTTTCTTCCCTGATTCACCG  
ATTTGGTCAGTGTGTGCCTCCTCCAGTCCACACTCTGCTGGCCAACTTCTATCTCCTCATTC  
CTCCAATCCTCAATCCCATTTGTCTATGCTGTTTCGCACCAAGCAGATCCGAGAGAGCCTTCT  
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

45

**AOLFR50 sequences:**

MNLD SFFSFLKSLIMALSNSSWRLPQPSFFLVGIPGLEESQHWIALPLGILYLLALVGNVTILFII  
WMDPSLHQSMYLFLSMLAAIDL VVASSTAPKALAVLLVRAQEIGYTVCLIQMFFTHAFSSMES  
GVLVAMALDRYVAICHPLHHSTILHPGVIGHIGMVVLVRGLLLIPFLILLRLKIFCQATIIGHAY  
50 CEHMAVVKLACSETTVNRAYGLTVALLVGLDVLAIGVSYAHILQAVLKVPGNEARLKAFST  
CGSHVCVILVFYIPGMFSFLTHRFGHHVPHHVHLLAILYRLVPPALNPLVYRVKTQKIHQ  
(SEQ ID NO: 95)

55 ATGAATTTGGATTCTTTTTTCTCTTTCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC  
CAGCTGGAGGCTACCCAGCCTTCTTTTTCTCCTGGTAGGAATCCGGGTTAGAGGAAAGC  
CAGCACTGGATCGCACTGCCCCGGGCATCCTTTACCTCCTTGCTCTAGTGGCAATGTGA

CCATTCTCTTCATCATCTGGATGGACCCATCCTTGCACCAATCTATGTACCTCTTCCTGTCC  
 ATGCTAGCTGCCATCGACCTGGTTGTGGCCTCCTCCACTGCACCCAAAGCCCTTGCAGTGC  
 TCCTGGTTTCGTGCCCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTTCACCCAT  
 GCATTCTCCTCCATGGAGTCAGGGGTACTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA  
 5 TTTGTACCCCTTGCACCATCCACAATCCTGCATCCAGGGGTCATAGGGCACATCGGAAT  
 GGTGGTGTGGTGCGGGGATTACTACTCCTCATCCCCCTTCTCATTCTGTTGCGAAAACCTT  
 ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAAC  
 TTGCCTGCTCAGAAACCACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGTGTTGGT  
 TGGGCTGGATGTCCTGGCCATTGGTGTTCCTATGCCACATTCTCCAGGCAGTGTGAAG  
 10 GTACCAGGAAATGAGGCCCCGACTTAAGGCCCTTAGCACATGTGGCTCTCATGTTTGTGTCA  
 TCCTGGTCTTCTATATCCCGGGAATGTTCTCCTTCTCACTCACCGCTTTGGTTCATCATGTA  
 CCCCATCACGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGTGCCACCTGCACTCAATCC  
 TCTTGTCTATAGGGTGAAGACCCAGAAGATCCACCAGTGA (SEQ ID NO: 96)

15 **AOLFR51 sequences:**

MCQQILRDCILLIHLHCINRKKVSLVMLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAM  
 YIIALLGNTIIVTAIWMDSTRHEPMYCFLCVLAADVIVMASSVVPKMVSIFCSGDSSISFSACFTQ  
 MFFVHLATAVETGLLLTMAFDTRYVAICKPLHYKRILTPQVMLGMSMAITIRAIATPLSWMVS  
 HLPFCGSNVVVHSYCEHIALARLACADVPSSLYSLIGSSLMVGSVAFIAASYILILKAVFGLSS  
 20 KTAQLKALSTCGSHVGVMALYYLPGMASIYAAWLQDQVPLHTQVLLADLYVIIPATLNPIIY  
 GMRTKQLRERIWSYLMHVLFDHNSLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA  
 AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC  
 25 CTTCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA  
 GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA  
 TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA  
 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG  
 CTTTAGTGCTTGTTTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG  
 30 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA  
 GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT  
 AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT  
 GTCCACTCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA  
 GCAGTCTCTACAGTCTGATTGGTTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT  
 35 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA  
 AGCATTAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG  
 GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACACCCAAGTCCTGC  
 TAGCTGACCTGTACGTGATCATCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC  
 CAAACAACCTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC  
 40 CTGGGTTTCATGA (SEQ ID NO: 98)

**AOLFR52 sequences:**

MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAMYITALLGNTLIVTAIWMDSTRHEPMY  
 CFLCVLAADVIVMASSVVPKMVSIFCSGDSSISFSACFTQMFFVHLATAVETGLLLTMAFDTRYV  
 45 AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMTPLSWMMNHLFPFCGSNVVVHSYCKHIALAR  
 LACADVPSSLYSLIGSSLMVGSVAFIAASYILILRAVFDLSSKTAQLKALSTCGSHVGVMALY  
 YLPGMASIYAAWLQDIVPLHTQVLLADLYVIIPATLNPIIYGMRTKQLLEGIWSYLMHFLFDH  
 SNLGS (SEQ ID NO: 99)

50 ATGCTGGGTCCAGCTTACAACCACACAATGGAAACCCCTGCCTCCTTCTCCTTGTGGGTA  
 TCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC  
 AGCCCTGTTAGGAAACACCTCATCGTGACTGCAATCTGGATGGATTCCACTCGGCATGAG  
 CCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTATGGCCTCCTCCGTGGT  
 ACCCAAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTGTTC  
 55 ACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATGG  
 CTTTGTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCACGCCTCA

AGTGATGCTGGGAATGAGTATGGCCGTCACCATCAGAGCTGTCACATTCATGACTCCACTG  
 AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTTGTCCACTCCTACTGTAA  
 GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCAGCAGTCTCTACAGTCTG  
 ATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCTGCCTCCTATATCTTAAT  
 5 TCTCAGGGCAGTATTTGATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAAGCACATGT  
 GGCTCCCATGTGGGGGTTATGGCTTTGTAATCTACCTGGGATGGCATCCATCTATGCGG  
 CCTGGTTGGGGCAGGATATAGTGCCTTGACACACCAAGTGCTGCTAGCTGACCTGTACGT  
 GATCATCCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAACAATTGCTGGAG  
 GGAATATGGAGTTATCTGATGCACTTCCTCTTTGACCACTCCAACCTGGGTTTCATGA (SEQ  
 10 ID NO: 100)

**AOLFR54 sequences:**

MSDSNLSDNHLPDTFFLTGIPGLEAAHFWIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY  
 LFLCLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMAFDRYVA  
 15 ICNPLRYTTILNHAIVIGRIGFVGLFRSVAIVSPFIFLLRRLPYCGHRVMTHTYCEHMGIA RLACA  
 NITVNIVYGLTVALLAMGLDSILIAISYGFILHAVFHLPSHDAQHKALSTCGSHIGIILVFYIPAFF  
 SFLTHRFGHHEVPKHVHIFLANLYVLVPPVLNPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID  
 NO: 101)

20 ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC  
 CAGGGCTGGAGGCTGCCCACCTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTTGTAGC  
 ACTGGTTGGAAATGCTGCCCTCATCCTGGTCATTGCCATGGACAATGCTCTTCATGCACCT  
 ATGTACCTCTTCTCTGCCTTCTCTCACTCACAGACCTGGCTCTCAGTTCTACCACTGTGCC  
 CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCCTTTGGTGGATGCCTGGCC  
 25 CAGATGTTTTGTGTCCATTCTATCTATGCTCTGGAGTCCCTCGATTCTACTTGCCATGGCCTT  
 TGATAGGTATGTGGCTATCTGTAACCCATTAAGGTATACAACCACTTCTCAACCATGCTGTC  
 ATAGGCAGAATTGGCTTTGTTGGGCTATTCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTT  
 CTTGCTGAGGCGACTCCCCTACTGTGGTCACCGTGTGATGACACACACATACTGTGAGCAT  
 ATGGGCATCGCCGACTGGCCTGTGCCAACATCACTGTCAATATTGTCTATGGGCTAACTG  
 30 TGGCTCTGCTGGCCATGGGACTGGATTCCATTCTCATTGCCATTTCCATATGGCTTTATCCTC  
 CATGCAGTCTTTCACCTTCCATCTCATGATGCCCAGCACAAAGCTCTGAGTACCTGTGGCT  
 CCCACATTGGCATCATCCTGGTTTTCTACATCCCTGCCTTCTTCTCCTTCCTACCCACCGC  
 TTTGGTCACCACGAAGTCCCAAGCATGTGCACATCTTTCTGGCTAATCTCTATGTGCTGG  
 TGCCTCCTGTACTCAATCCTATTCTCTATGGAGCTAGAACCAAGGAGATTCCGAGTCGACT  
 35 TCTAAACTGCTTCACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

**AOLFR57 sequences:**

MSFQVTYMFYLHWTMEKSNNSTLFILLGFSQNKNIENVLCFVLFVLCYIAIWMGNLLIMISITCTQ  
 LIHQPMYFFLNYLSLSDLCYTSTVTPKLMVDLLAERKTISYNNCMIQLFTTHFFGGIEIFILTM  
 40 AYDRYVAICKPLHYTHMSRQKCNTHIVCCTGGFIHSASQFLLTIFVPFCGPNEIDHYFCDVYPLL  
 KLACSNHIMIGLLVIANSGLIALVTFVLLLSYVFILYTIRAYSAERRSKALATCSSHVIVVVLFF  
 APALFIYIRPVTTFSEDKVLFYTHAPMFNPLIYTLRNTEMKNAMRKVWCCQILLKRNQLF  
 (SEQ ID NO: 103)

45 ATGTCATTTACAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAGCAATAATA  
 GCACCTTTGTTTATTCTCTTGGGGTTTTCCCAAATAAGAACATTGAAGTCCTCTGCTTTGTA  
 TTATTTTTGTTTTGCTACATTGCTATTTGGATGGGAACTTACTCATAATGATTTCTATCAC  
 GTGCACCCAGCTCATTACCAACCCATGTATTTCTTCCTCAATTACCTCTCACTCTCCGACC  
 TTTGCTACACATCCACAGTGACCCCCAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC  
 50 CATTTCTATAATAACTGTATGATACAACTCTTTACCACCCATTTTTTTGGAGGCATAGAGA  
 TCTTCATTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTTGCAAGCCCCCTGCACTA  
 CACCATTATTATGAGCAGGCAAAAGTGTAACACAATCATCATAGTTTGTGTACTGGGGGA  
 TTTATACATTCTGCCAGTCAGTTTCTTCTCACCATCTTTGTACCATTTTGTGGCCCAAATGA  
 GATAGATCACTACTTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA  
 55 TGATAGGTCTCTTAGTCATTGCTAATTCAGGCTTAATTGCTTTGGTGACATTTGTTGTCTTG  
 TTGTTGTCTTATGTTTTTATATTGTATACCATCAGAGCATACTCTGCAGAGAGACGCAGCA

AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCCTGTTTTTGTCTCCTGCATTG  
TTCATTTACATTAGACCGGTCAACATTCTCAGAAGATAAAGTGTTTGCCTTTTTTATAC  
CATCATTGCTCCCATGTTCAACCCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC  
GCCATGAGGAAAGTGTGGTGTGTCAAATACTCCTGAAAAGAAATCAACTTTTCTGA (SEQ  
ID NO: 104)

**AOLFR58 sequences:**

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF  
VLLGLSQPNVQEIVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI  
TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL  
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCPLYLLELACTDTHIFGLMVVINSF  
FICIINFSLLLVSAYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA  
AIFYIILNPLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 105)

ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCCTTGGATGTACCAACTTGTTAA  
TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCTTTGTCTAATTGCAGACTATA  
CATGATCCCTGTTGGAGCTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA  
ACTGAGTTTGTCTCCTCGGGACTTTCACAGAATCCAAATGTTTCAGGAAATAGTATTTGTG  
TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATTCTC  
AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGTCTTCTGGA  
TGCGTGCTTCTCATCTGTCATACCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA  
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG  
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA  
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG  
GGCCTCTTGCAATCCATGATACAAATCTTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA  
TGTCATCAATCACTTTATGTGTGACTGTACCCGTTACTGGAGCTTGCTGCACTGATACTC  
ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG  
TTGCTTGTCTCCTATGCTGTCATCTTGTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG  
GAAAGCTCTCTCCACCTGTGGATCTCATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA  
TATTTGTATATACACGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT  
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC  
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA  
AACTTTAA (SEQ ID NO: 106)

**AOLFR59 sequences:**

MGDWNNSDAVEPIFILRGFPGLEYVHSWLSILFCLAYLVAFMGNVTILSVIWISSLHQPMYYFI  
SILAVNDLGMSLSTLPTMLAVLWDAPEIQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH  
PLHYPTILNSVIGKIGLACLLRSLGVVLPPLLLRHYHYCHGNALSHAFCLHQDVLRLSCTDA  
RTNSIYGLCVVIATLGVDSIFILLSYVLILNTVLDIASREEQLKALNTCVSHICVVLIFVPVIGVS  
MVHRFGKHLSPIVHILMADIYLLPVLNPIVYSVRTKQIRLGILHKFVLRRRF (SEQ ID NO:  
107)

ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTTCTG  
GACTGGAGTATGTTCACTTCTGGCTCTCCATCCTCTTCTGTCTTGCAATTTGGTAGCATTT  
ATGGGTAATGTTACCATCCTGTCTGTCATTTGGATAGAATCCTCTCTCCATCAGCCCATGTA  
TTACTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTCCCACCA  
TGCTTGCTGTGTTATGGTTGGATGCTCCAGAGATCCAGGCAAGTGCTTGCTATGCTCAGCT  
GTTCTTCATCCACACATTCACATTCCTGGAGTCTCAGTGTTGCTGGCCATGGCCTTTGACC  
GTTTTGTTGCTATCTGCCATCCACTGCACTACCCCAACCATCCTCACCAACAGTGTAATTGGC  
AAAATTGGTTTGGCCTGTTTGCTACGAAGCTTGGGAGTTGTACTTCCCACACCTTTGCTACT  
GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTCACGCCTTCTGTTTGCACCAGGAT  
GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA  
TTGCCACACTAGGTGTGGATTCAATCTTCATACTTCTTTCTTATGTTCTGATTCTTAATACT  
GTGCTGGATATTGCATCTCGTGAAGAGCAGCTAAAGGCACTCAACACATGTGTATCCCATA  
TCTGTGTGGTGCTTATCTTCTTTGTGCCAGTTATTGGGGTGTCAATGGTCCATCGCTTTGGG  
AAGCATCTGTCTCCCATAGTCCACATCCTCATGGCAGACATCTACCTTCTTCTTCCCCCAGT

CCTTAACCCTATTGTCTATAGTGTGTCAGAACAAAGCAGATTTCGTCTAGGAATTCTCCACAAG  
TTTGTCTTAAGGAGGAGGTTTAA (SEQ ID NO: 108)

**AOLFR60 sequences:**

5 MFLPNDTQFHPSSFLLLGIPGLETLHIWIGFPFCVYMIALIGNFTILLVIKTDSSLHQPMFYFLA  
MLATTDVGLSTATIPKMLGIFWINLRGIIFEACLTQMFFIHNFTLMESAVLVAMAYDSYVAICN  
PLQYSAILTNKVSVIGLGVFVRALIFVIPILLSILLRPFNGHVIPHTYCEHMGHLASCAIKINI  
IYGLCAICNLVFDITVIALSYVHILCAVFRLPHEPRLKSLSTCGSHVCVILAFYTPALFSFMTHC  
FGRNVPRYIHILLANLYVVVPPMLNPVIYGVRTKQIYKCVKKILLQEQQMEKEEYLHTRF  
10 (SEQ ID NO: 109)

ATGTTTCCTTCCCAATGACACCCAGTTTCACCCCTCCTTCTGTTGCTGGGGATCCCAGG  
ACTAGAAACACTTCACATCTGGATCGGCTTTCCCTTCTGTGCTGTGTACATGATCGCACTC  
ATAGGGAACCTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCCTACACCAGCCCATGT  
15 TCTACTTCTGGCCATGTTGGCCACCACTGATGTGGGCTCTCTCAACAGCTACCATCCCTAA  
GATGCTTGGAATCTTCTGGATCAACCTCAGAGGGATCATCTTTGAAGCCTGCCTCACCCAG  
ATGTTTTTTATCCACAACCTTCACTTATGGAGTCAGCAGTCCTTGTGGCAATGGCTTATG  
ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCCTACCAACAAGGTTGT  
TTCTGTGATTGGTCTTGGTGTGTTTGTGAGGGCTTTAATTTTCGTCATTCCCTCTATACTTC  
20 TTATATTGCGGTTGCCCTTCTGTGGGAATCATGTAATTCCCCACACCTACTGTGAGCACAT  
GGGTCTTGCTCATCTATCTTGTGCCAGCATCAAAATCAATATTATTATGTTTATGTGCCA  
TTTGTAATCTGGTGTGTTGACATCACAGTCATTGCCCTCTCTTATGTGCATATTCTTTGTGCT  
GTTTTCCGTCTTCTACTCATGAGCCCCGACTCAAGTCCCTCAGCACATGTGGTTCACATGT  
GTTGTGTAATCCTTGCTTCTATACACCAGCCCTCTTTTCTTTATGACTCATTGCTTTGGCC  
25 GAAATGTGCCCCGCTATATCCATATACTCCTAGCCAATCTCTATGTTGTGGTGCCACCAAT  
GCTCAATCCTGTCATATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAT  
ATTATTGCAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA  
(SEQ ID NO: 110)

**AOLFR61 sequences:**

30 MSIINTSYVEITTFVLVGMPLGLEYAHIWISIPICSMYLIAILNGTILFIKTEPSLHGPMYYFLSML  
AMSDLGLSSLPTVLSIFLNPETSSSACFAQEFFIHGFSVLESSVLLIMSFDRLAIHNPLRYT  
SILTTVRVAQIGIVFSFKSMLLVLPFPFTLRLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY  
GFFGALCLMVDFILIAVSYTLILKTVPGIASKKEELKALNTCVSHICAVIIFYLPIINLAVVHRFAG  
35 HVSPLINVLMANVLLLVPPLMKPIVYCVKTKQIRVRVAKLCQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG  
GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT  
CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCATTGT  
40 ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCCACT  
GTGTTAAGCATCTTCTGTTCAATGCCCTGAAACTTCTTCTAGTGCCTGCTTTGCCCAGGA  
ATTCTTCATTGATGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCAATTGATA  
GATTCCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC  
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT  
45 TAAGAAGCTTGAGATATTGCAAGAAAAACCAATTATCCCATTCTACTGTCTCCACCAGGA  
TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA  
CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT  
ACCGGGAATTGCATCCAAAAGGAGGAGCTTAAGGCTCTCAATACTTGTGTTTACACATC  
TGTGCAAGTATCATCTTCTACCTGCCCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG  
50 GCATGTCTCTCCCCTCATTAAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCGCTGA  
TGAAACCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT  
GTGTCAATGGAAGATTAA (SEQ ID NO: 112)

**AOLFR62 sequences:**

55 MFYHNKSIFHPVTFFLIGIPGLEDFHWMISGPFCSVYLVALLGNATILLVIKVEQTLREPMFYFL  
AILSTIDLALSATSVPRMLGIFWFDAHEINYGACVAQMFLIHAFTGMEAEVLLAMAFDRYVAIC



APLHYATILTSVLVGISMCIIVIRPVLLTLP MVYLIYRLPFCQAHIIAHSYCEHMGIAKLSCGNIRI  
NGIYGLFVVSFFVLNLVLIGISYVYILRAVFRLP SHDAQLKALSTCGAHVGVICVFYIPSVFSFLT  
HRFGHQIPGYIHILVANLYLIIPPSLNP IYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

5 ATGTTTTATCACACAAGAGCATATTTACCCAGTCACATTTTCTCATTGGAATCCCAGG  
TCTGGAAGACTTCCACATGTGGATCTCCGGGCCCTTCTGCTCTGTTACCTTGTGGCTTTGC  
TGGGCAATGCCACCATTCTGCTAGTCATCAAGGTAGAACAGACTCTCCGGGAGCCCATGTT  
CTACTTCTGGCCATTCTTTCCACTATTGATTTGGCCCTTTCTGCAACCTCTGTGCCTCGCA  
TGCTGGGTATCTTCTGGTTTGATGCTCACGAGATTA ACTATGGAGCTTGTGTGGCCCAGAT  
10 GTTCTGATCCATGCCTTCACTGGCATGGAGGCTGAGGTCTTACTGGCTATGGCTTTTGAC  
CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATCTTGACATCCCTAGTGTGGT  
GGGCATTAGCATGTGCATTGTAATTCGTCCCGTTTTACTTACACTTCCCATGGTCTATCTTA  
TCTACCGCTACCCCTTTTGTGAGGCTCACATAATAGCCCATTCCTACTGTGAGCACATGGG  
CATTGCAAAATTGTCCTGTGGAAACATTGCTATCAATGGTATCTATGGGCTTTTGTAGTTT  
15 CTTTCTTTGTTCTGAACCTGGTGCTCATTGGCATCTCGTATGTTTACATTCTCCGTGCTGTC  
TTCCGCCTCCCATCACATGATGCTCAGCTAAAAGCCCTAAGCACGTGTGGCGCTCATGTTG  
GAGTCATCTGTGTTTTCTATATCCCTTCAGTCTTCTCTTTCCTTACTCATCGATTGGACAC  
CAAATACCAGGTTACATTCACATTCTTGTGCAATCTCTATTTGATTATCCACCCTCTCT  
CAACCCCATCATTTATGGGGTGAGGACCAACAGATTGAGAGCGAGTGCTCTATGTTTTT  
20 ACTAAAAAATAA (SEQ ID NO: 114)

**AOLFR63 sequences:**

MSINTSYVEITTFVLVGMPLGLEYAHIWISIPICSMYLIAILGNGTILFIKTEPSLHEPMYYFLSML  
AMSDLGLSLSSLPTVLSIFLNAPEISSNACFAQEFFIHGFSVLESSVLLIMSFDRLAIHNPLRYTS  
25 ILTTVRVAQIGIVFSFKSMLLVLPFPFTLRNLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY  
GFFGALCLMVDFILIAVSYTLILKTVLGIASKKEQLKALNTCVSHICAVIIFYLPIINLAVVHRFAR  
HVSPLINVL MANVLLVPPLTNPIVYCVKTKQIRVRVAKLCQRKI (SEQ ID NO: 115)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG  
30 GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT  
CTAGGAAATGGCACCATTCTTTTTATCATCAAGACAGAGCCCTCCTTGCATGAGCCCATGT  
ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT  
GTGTAAAGCATCTTCTGTTCAATGCTCCTGAAATTTCAATCAATGCCTGCTTTGCCCAGGA  
ATTCTTCATTCATGGATTCTCAGTACTGGAGTCTCAGTCTCCTGATCATGTCAATTTGATA  
35 GATTCTAGCCATCCACAACCTCTGAGATACACCTCAATCCTGACAACCTGTCAGAGTTGC  
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT  
TAAGAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA  
TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTGGAGCA  
CTCTGCCTTATGGTAGACTTTATTTCTATTGCTGTGCTTACACCCTGATCCTCAAGACTGT  
40 ACTGGGAATTGCATCCAAAAAGGAGCAGCTTAAGGCTCTCAATACTTGTGTTTCACACATC  
TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG  
GCATGTCTCTCCCTCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGA  
CGAACCCAATTGTTTATTGTGTA AAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT  
GTGTCAACGGAAGATTAA (SEQ ID NO: 116)

45

**AOLFR64 sequences:**

MTILLNSSLQRATFFLTGFQGLEGLHGWISIPFCFIYLT VILGNLTILHVICTDATLHGPMYYFLG  
MLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPL  
HDSTVLTPACIVKMGLSSVLR SALLILPLPFLKRFQYCHSHVLAHAYCLHLEIMKLACSSIIVN  
50 HIYGLFVVACTVGVDLLIFLSYALILRTVLSIASHQERLRALNTCVSHICAVLLFYIPMIGLSLV  
HRFGEHLPRVVHLFMSYVYLLVPPLMNP IYSIKTKQIRQRIKKFQFIKSLRCFWKD (SEQ ID  
NO: 117)

ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTTCTTCTGACGGGCTTCCAAG  
55 GTCTAGAAGGTCTCCATGGCTGGATCTCTATCCCTTCTGCTTCATCTACCTGACAGTTATC  
TTGGGGAACCTACCATCTCCACGTCATTTGTACTGATGCCACTCTCCATGGACCCATGT

ACTATTTCTTGGGCATGCTAGCTGTCACAGACTTAGGCCTTTGCCTTTCCACACTGCCCCT  
 GTGCTGGGCATTTTCTGGTTTGATACCAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGC  
 TCTTCTTCATCCACACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGAC  
 CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCTGACACCTGCATGTATTG  
 5 TCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCCTTGCCATTCCCT  
 CTGAAGCGCTTCCAATACTGCCACTCCCATGTGCTGGCTCATGCTTATTGTCTTCACCTGGA  
 GATCATGAAGCTGGCCTGCTCTAGCATCATTGTCAATCACATCTATGGGCTCTTTGTTGTG  
 GCCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTTCTCTCATACGCCCTCATCTTCGCAC  
 CGTGCTCAGCATTGCCTCCCACCAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT  
 10 ATCTGTGCTGTACTGCTCTTCTACATCCCCATGATTGGCTTGTCTCTTGTGCATCGCTTTGG  
 TGAACATCTGCCCGCGTTGTACACCTCTTCATGTCTATGTGTATCTGTGTTACACCCC  
 TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTCGCCAGCGCATCATTAAAGAA  
 GTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGAAGGATTAA (SEQ ID NO: 118)

15 **AOLFR65 sequences:**

MAGRMSTSNHTQFHPSSFLLLGIPGLEDVHIWIGVPFFVYLVALLGNTALLFVIQTEQSLHEPM  
 YYFLAMLDLGLSTATIPKMLGIFWNTKEISFGGCLSHMFFIHFFTAMESIVLVAMAFDRYI  
 AICKPLRYTMILTSKIHSLIAGIIVLRSLYMVVPLVFLLLRLPFCGHRIIPHTYCEHMGARLACAS  
 IKVNIRFGLGNISLLLDVILILSYVRILYAVFCLPSWEARLKALNTCGSHIGVILAFFTPAFFSFL  
 20 THRFGHNIPQYIHILANLYVVVPPALNPVIYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCCATCCTTCTTCATTCTACTGCT  
 GGGTATCCCAGGGCTAGAAGATGTGCACATTTGGATTGGAGTCCCTTTTTCTTTGTGTAT  
 CTTGTTGCACTCCTGGGAAACACTGCTCTCTTGTGTTGTGATCCAGACTGAGCAGAGTCTCC  
 25 ATGAGCCTATGTACTACTTCTGCGCATGTTGGATTCCATTGACCTGGGCTTGTCTACAGC  
 CACCATCCCCAAAATGTTGGGCATCTTCTGGTTCAATACCAAAGAAATATCTTTTGGAGGC  
 TGCCTTTCTCACATGTTCTTCATCCATTTCTTCACTGCTATGGAGAGCATTGTGTTGGTGGC  
 CATGGCCTTTGACCGCTACATTGCCATTTGCAAACCTCTTCGGTACACCATGATCCTCACCA  
 GCAAATCATCAGCCTCATTGCAGGCATTGCTGTCCTGAGGAGCCTGTACATGGTTGTTCC  
 30 ACTGGTGTTTCTCCTTCTGAGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTTATT  
 GTGAGCACATGGGCATTGCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTTTGG  
 CTTGGCAACATATCTCTCTTGTACTGGATGTTATCCTTATTCTCTCCTATGTCAGGA  
 TCCTGTATGCTGTCTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGT  
 GGTCTCATATTGGTGTTATCTTAGCCTTTTTTACACCAGCATTTTTTTCACTTCTTGACACA  
 35 TCGTTTTGGCCATAATATCCACAGTATATACATATTATATTAGCCAACTGTATGTGGTTG  
 TCCACACAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTTCGAGAGAGAG  
 TGCTGAGGATTTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

40 **AOLFR66 sequences:**

MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDEALHRPMYVFL  
 ALLSFTDVLMTSTLPNTLFILWFNLKEIDFKACLAQMFFVHTFTGMESGVLMLMALDHCVAI  
 CFPLRYATILTNSVIAKAGFLTFLRGVMLVIPSTFLTKRLPYCKGNVIPHTYCDHMSVAKISCGN  
 VRVNAIYGLIVALLIGGFDILCITISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLTYVPAFF  
 TFFTHHFGGHTIPLHIHILMANLYLLMPPTMNPVYGVKTRQVRESVIRFFLKGDNSHNF (SEQ  
 45 ID NO: 121)

ATGTCATTTCTAAATGGCACCAGCCTAACTCCAGCTTCATTATCCTAAATGGCATCCCTG  
 GTTTGGAAGATGTGCATTTGTGGATCTCCTTCCCACTGTGTACCATGTACAGCATTGCTATT  
 ACAGGGAACCTTCGGCCTTATGTACCTCATCTACTGTGATGAGGCCTTACACAGACCTATGT  
 50 ATGTCTTCTTGCCTTCTTTCTTTCACAGATGTGCTCATGTGCACCAGCACCCTTCCCAAC  
 ACTCTCTTCATATTGTGGTTTAATCTCAAGGAGATTGATTTTAAAGCCTGCCTCGCCAGAT  
 GTTCTTTGTGCACACCTTACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGAC  
 CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCCTCACTAATTCAGTCATTGC  
 TAAAGCTGGGTTCTCACTTTTCTTAGGGGTGTGATGCTTGTTATCCCTTCCACTTTCCTCA  
 55 CCAAGCGCCTTCCATACTGCAAGGGCAACGTCATACCCACACCTACTGTGACCACATGTC  
 TGTGGCCAAGATATCTTGTGGTAATGTGAGGGTTAACGCCATCTATGGTTTGATAGTTGCC

CTGCTGATTGGGGGCTTTGATATCCTGTGCATTACAATCTCCTACACTATGATTCTTCAAGC  
AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCTTCAGCACCTGCACTGCCCCAC  
TTCTGTGCCATAGTCCTCACCTATGTTCCAGCCTTCTTTACCTTCTTTACACACCATTTTGG  
GGGACACACCATTCCTCTACACATACATATTATTATGGCTAATCTCTACCTACTAATGCCTC  
5 CCACAATGAACCCTATTGTGTATGGGGTGAAAACCAGGCAGGTACGAGAAAAGTGTCATTA  
GGTTCTTTCTTAAGGGAAAGGACAATTCTCATAACTTTTAA (SEQ ID NO: 122)

**AOLFR67 sequences:**

10 MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYIIAVVGNCGLICLISHEEALHRPMYYFLA  
LLSFTDVTLCCTTMVPMNMLCIFWFNLKEIDFNACLAQMFFVHMLTGMESGVLMLMALDRYVAI  
CYPLRYATILNPNVIAKAGLATFLRNVMLIIPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN  
FKVNAIYGLMVALLIGVFDICISVSYTMILQAVMSLSSADARHKAFSTCTSHMCSIVITYVAAP  
FTFFTHRFVGHNPNIHIIIVANLYLLLPTMNPVYGVKTKQIQEGVIKFLGDKVSFTYDK  
(SEQ ID NO: 123)

15 ATGTCTGGGGACAACAGCTCCAGCCTGACCCCAGGATTCTTTATCTTGAATGGCGTTCCTG  
GGCTGGAAGCCACACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTGCTGTC  
GTGGGGAACTGTGGGCTCATCTGCCTCATCAGCCATGAGGAGGGCCCTGCACCGGCCCATGT  
ACTACTTCCTGGCCCTGCTCTCCTTCACTGATGTCACCTTGTCACCACCATGGTACCTAAT  
20 ATGCTGTGCATATTCTGGTTCAACCTCAAGGAGATTGACTTTAACGCCTGCCTGGCCCA  
TGTTTTTTGTCCATATGCTGACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGA  
CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCCTTACCAACCCTGTCATCG  
CCAAGGCTGGTCTTGCCACCTTCTTGAGGAATGTGATGCTCATCATCCCATTCACCTCTCCTC  
ACCAAGCGCCTGCCCTATTGCCGGGGGAACCTTCATCCCCCACACCTACTGTGACCATATGT  
25 CTGTGGCCAAGGTATCCTGTGGCAATTTCAAGGTCAATGCTATTTATGGTCTGATGGTTGC  
TCTCCTGATTGGTGTGTTTGATATCTGCTGTATCTCTGTATCTTACACTATGATTTTGCAGG  
CTGTTATGAGCCTGTCATCAGCAGATGCTCGTCACAAAGCCTTCAGCACCTGCACATCTCA  
CATGTGTTCCATTGTGATCACCTATGTTGCTGCTTTTTTCACTTTTTTCACTCATCGTTTTGT  
AGGACACAATATCCCAAACCACATACACATCATCGTGGCCAACCTTTATCTGCTACTGCCT  
30 CCTACCATGAACCAATTGTTTATGGAGTCAAGACCAAGCAGATTGAGGAAGGTGTAATTA  
AATTTTTACTTGGAGACAAGGTTAGTTTTACCTATGACAAATGA (SEQ ID NO: 124)

**AOLFR68 sequences:**

35 MTTHRNDTLSTEASDFLLNCFVRSPSWQHWLSLPLSLLFLLAVGANTTLLMTIWLEASLHQPL  
YYLLSLLSLLDIVLCLTVIPKVLTFWFDLRPISFPACFLQMYIMNCF LAMESCTFMVMAYDRY  
VAICHPLRYPSTHDHFVVKAAAMFILTRNVLMTLPIPILSAQLRYCGRNVIENCICANMSVSRLSC  
DDVTINHL YQFAGGWTL LGS DLILIFLSYTFILRAVRLKAEGAVAKALSTCGSHFMLILFFSTIL  
LVFVLTHVAKKKVSPDVPVLLNVLHHVIPAALNPIYGVRTQEIKQGMQRLLKKGC (SEQ ID  
NO: 125)

40 ATGACAACACACCGAAATGACACCCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT  
TTGTGAGATCCCCCAGCTGGCAGCACTGGCTGTCCCTGCCCCTCAGCCTCCTTTTCTCTTG  
GCCGTAGGGGCCAACACCACCCTCCTGATGACCATCTGGCTGGAGGCCTCTCTGCACCAGC  
CCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGGACATCGTGCTCTGCCTCACTGTCATC  
45 CCAAGGTCTGACCATCTTCTGGTTTGACCTCAGGCCCATCAGCTTCCCTGCCTGCTTCTCCT  
CCAGATGTACATCATGAATTGTTTCTAGCCATGGAGTCTTGACATTCATGGTCATGGCC  
TATGATCGTTATGTAGCCATCTGCCACCCACTGAGATATCCATCAATCATCACTGATCACTT  
TGTAGTCAAGGCTGCCATGTTTATTTTGACCAGAAATGTGCTTATGACTCTGCCCATCCCC  
ATCCTTTTCAGCACAACTCCGTTATTGTGGAAGAAATGTCATTGAGAACTGCATCTGTGCCA  
50 ATATGTCTGTTTCCAGACTCTCCTGCGATGATGTCACCATCAATCACCTTTACCAATTTGCT  
GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTTCTCTCTACACCTTCATTCT  
GCGAGCTGTGCTGAGACTCAAGGCAGAGGGTGCCGTGGCAAAGGCCCTAAGCACATGTGG  
CTCCCACTTCATGCTCATCCTCTTCTTACAGCACCATCCTTCTGGTTTTTGTCTCACACATGT  
GGCTAAGAAGAAAGTCTCCCTGATGTGCCAGTCTTGCTCAATGTTCTCCACCATGTCATT  
55 CCGTGCAGCCCTTAACCCCATCATTTACGGGGTGAGAACCCAAGAAATTAAGCAGGGAATG  
CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

**AOLFR69 sequences:**

MSYSIYKSTVNIPLSHGVVHSFCHNMNCNFMHIFKFLVDFNMKNVTEVTLFVLKGFTDNLELQ  
TIFFFLFLAIYLFITLMGNLGLILVVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN  
5 KVISFLGCVAQVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVSMSPRVYVIMPLINASYVAGI  
LHATIHVATFSLFCGANEIRRVFCDDIPLLAISYSDHTNQLLLFYFVGSIELVTILIVLISYGLIL  
LAILKMYSAGEGRRKVFTSCGAHLTGVSIIYYGTILFMYVRPSSSYASDHDMIVSIFYTIVIPLLNPV  
IYSLRNKDVKDSMKKMFQKQVINKVYFHTKK (SEQ ID NO: 127)

10 ATGTCGTACAGTATATACAAGAGCACAGTTAACATCCCCTTGAGTCATGGTGTGTTTCATT  
CTTTTTGTGATAATATGAACTGTAACCTTATGCATATCTTCAAGTTTGTCTAGATTTC AAC  
ATGAAGAATGTCACGTGAAGTTACCTTATTTGACTGAAGGGCTTCACAGACAATCTTGAAC  
TGCAGACTATCTTCTTCTTCTGTTTCTAGCAATCTACCTCTTCACTCTCATGGGAAATTTA  
GGACTGATTTTAGTGGTCATTAGGGATTCCCAGCTCCACAAACCCATGTACTATTTTCTGA  
15 GTATGTTGTCTTCTGTGGATGCCTGCTATTCCCTCAGTTATTACCCCAAATATGTTAGTAGAT  
TTTACGACAAAGAATAAAGTCATTTTCATTCTTGGATGTGTAGCACAGGTGTTTCTTGCTT  
GTAGTTTTGGAACACAGAATGCTTTCTTGGCTGCAATGGCTTATGATCGCTATGTAGC  
CATCTACAACCCCTCTCCTGTATTACGTGAGCATGTCAACCAGAGTCTACATGCCACTCATC  
AATGCTTCTCTATGTTGCTGGCATTTCATGCTACTATACATACAGTGGCTACATTTAGCCT  
20 ATCCTTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTTGTGATATCCCTCCTCTCCTTGCTA  
TTTCTTATTCTGACACTCACACAAACCAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG  
CTGGTCACTATCCTGATTGTTCTGATCTCCTATGGTTTGATTCTGTTGGCCATTCTGAAGAT  
GTATTCTGCTGAAGGGAGGAGAAAAGTCTTCTCCACATGTGGAGCTCACCTAACTGGAGT  
GTCAATTTATTATGGGACAATCCTCTTCATGTATGTGAGACCAAGTCCAGCTATGCTTCG  
25 GACCATGACATGATAGTGTCAATATTTTACACCATTGTGATTCCCTTGCTGAATCCCGTCAT  
CTACAGTTTGAGGAACAAAGATGTAAAAGACTCAATGAAAAAATGTTTGGGAAAAATCA  
GGTTATCAATAAAGTATATTTTCATACTAAAAAATAA (SEQ ID NO: 128)

**AOLFR70 sequences:**

30 MDSTFTGYNLYNLQVKTEMDKLSSGLDIYRNPLKNKTEVTMFILTGFTDDFELQVFLFLFFAI  
YLFTLIGNLGLVVLVIEDSWLHNPMMYYFLSVLSFLDACYSTVVPKMLVNFLAKNKSISFIGCA  
TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVSMSPRVYVPLITASVYAGILHATHIVA  
TFSLFCGANEIRRVFCDDIPLLAISYSDHTNQLLLFYFVGSIEIVTILIVLISCDIFILLSILKMHS  
KGRQKAFSTCGSHLTGVTIYHGTLVSYMRPSSSYASDHDIIVSIFYTIVIPKLNPIIYSLRNKEVK  
35 KAVKKMLKLVIYK (SEQ ID NO: 129)

40 ATGGACTCCACTTTTCACAGGCTATAACCTTTATAACCTGCAAGTAAAAACTGAAATGGACA  
AGTTGTGATCAGGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAGTCACCA  
TGTTTATATTGACAGGCTTCACAGATGATTTTGAGCTGCAAGTCTTCTATTTTACTATTT  
TTTGCAATCTATCTTTACCTTGATAGGCAATTTAGGGCTGGTTGTGTTGGTCATTGAGG  
ATTCCTGGCTCCACAACCCCATGTATTATTTTCTTAGTGTTTTATCATTCTTGGATGCTTGC  
TATTCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCTTGGCAAAAAATAAATCCATTT  
CATTATCGGATGTGCAACACAGATGCTTCTTTTGTACTTTTGGAACTACAGAATGTTTT  
CTCTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCCCTCTCCTGTATTTCAGT  
45 GAGCATGTCAACCCAGAGTCTATGTGCCACTCATCACTGCTTCTACGTTGCTGGCATTTTAC  
ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCCTTCTGTGGATCCAATGAAATTAG  
GCATGTCTTTTGTGATATGCCTCCTCTCCTTGCTATTTCTTGTCTGACACTCACACAAACC  
AGCTTCTACTCTTCTACTTTGTGGGTTCTATTGAGATAGTCACTATCCTGATTGTCCTCATT  
TCCTGTGATTTCACTCTGTTGTCCATTCTGAAGATGCATTCTGCTAAGGGAAGGCAAAAGG  
50 CCTTCTCTACATGTGGCTCTCACCTAACTGGAGTGACAATTTATCATGGAACAATTCTCGTC  
AGTTATATGAGACCAAGTCCAGCTATGCTTCAGACCATGACATCATAGTGTCAATATTTT  
ACACAATTGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAAA  
AAAGGCAGTGAAGAAAATGTTGAAATTGGTTTACAAATGA (SEQ ID NO: 130)

**AOLFR71 sequences:**

MGRNRNTNVPDFILTGLSDSEEVQMALFILFLIYLITMLGNVGMILIRLDLQLHTPMYFFLTH  
LSFIDLSYSTVITPKTLANLLTSNYISFMGCFAQMFFVFLGAAECFLSSMAYDRYVAICSPRLY  
PVIMSKRLCCALVTGPYVISFINSFVNVVWMSRLHFCDNSVVRHFFCDTSPILALSCMDTYDIEI  
5 MIHILAGSTLMVSLITISASYVSILSTILKINSTSGKQKALSTCASHLLGVTIFYGTMIFTYLPKPK  
SYSLGRDQVASVFYTVIPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

ATGGGTAGAAAGAAATAACACAAATGTGCCTGACTTCATCCTTACGGGACTGTCAGATTCTG  
AAGAGGTCCAGATGGCCCTCTTTATACTATTTCTCCTGATATACCTAATTACTATGCTGGGC  
10 AATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATTTT  
TCCTTACTCACTTGTCAATTTATTGACCTCAGTTACTCAACTGTCATCACACCTAAAACCTTA  
GCGAACTTACTGACTTCCAACATATATTTCTTCATGGGCTGCTTTGCCAGATGTTCTTTTT  
TGTCTTCTTGGGAGCTGCTGAATGTTTTCTTCTCTCATCAATGGCCTATGATCGCTACGTAG  
CTATCTGCAGTCCCTCTACGTTACCCAGTTATTATGTCCAAAAGGCTGTGTTGCGCTCTTGTC  
15 ACTGGGCCCTATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC  
TGCATTTCTGCGACTCAAATGTAGTTCGTCACTTTTTCTGCGACACGTCTCCAATTTTAGCT  
CTGTCTGCTGACATGACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCCACCC  
TGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTTACCATCCTGAAA  
ATTAATTCCACTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCCTCTCATCTCTTGGGAG  
20 TCACCATCTTTTATGGAATATGATTTTTACTTATTTAAACCAAGAAAGTCTTATTCTTTG  
GGAAGGGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCATGCTGAATCCACTCAT  
TTATAGTCTTAGAAACAAAGAAGTTAAAAATGCTCTCATTAGAGTCATGCAGAGAAGACA  
GGACTCCAGGTAA (SEQ ID NO: 132)

**AOLFR72 sequences:**

MAPENFTRVTEFILTVSSCPQLIPLFLVFLVLYGLTMAGNLGIITLTSVDSRLQTPMYFFLQHL  
ALINLGNSTVIAPKMLINFLVKKKTTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL  
YMVVVSRRLLCLLVSLTYLYGFSTAIVVSSYVFSVSYCSSNIINHFCYCDNVPLLALSCSDTYLPE  
TVVFISAATNVVGSLLIIVLVSYFNIVLSILKICSSEGRKKAFSTCASHMMAVTIFYGTLLFMYVQP  
30 RSNHSLDTHDDKMASVFYTLVIPMLNPLIYSLRNKDVKTALQRFMTNLCYSFKTM (SEQ ID NO:  
133)

ATGGCTCCTGAAAATTTACCAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC  
CAGAGCTCCAGATCCCCCTCTTCTGGTCTTTCTGGTGTCTATGGGCTGACCATGGCAGG  
35 GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCCATGTACTTTT  
TCCTGCAACATCTGGCTCTCATTAACTCTGGTAACTCTACTGTCAATGCCCTAAAATGCTG  
ATTAACTTTTTAGTAAAGAAGAAAACCTCATCTATGAATGTGCCACCCAACTGGGAG  
GGTTCTTGTTCTTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCCTGTGACCGCTAT  
GTGGCTATTTGTAACCTCTGCTGTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGCT  
40 GGTCTCCCTCACATACCTCTATGGCTTTCTACAGCTATTGTGGTTTCATCTTATGTATTCT  
CTGTGTCTTATTGCTCTTCTAATAATAATCAATCATTTTTACTGTGATAATGTTCTCTGTTA  
GCATTATCTTGCTCTGATACTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA  
ATGTGGTTGGTTCCTTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTTGTCTATTTTA  
AAAATATGTTTCATCAGAAGGAAGGAAAAAAGCCTTTTCTACCTGTGCTTCACATATGATGG  
45 CAGTCACAATTTTTTATGGGACATTGCTATTCTATGTATGTGCAGCCCCGAAGTAACCATTC  
ATTGGATACTGATGATAAGATGGCTTCTGTGTTTTACACGTTGGTAATTCCTATGCTGAAT  
CCCTTGATCTACAGCCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTTCATGACA  
AATCTGTGCTATTCTTTAAACAATGTAA (SEQ ID NO: 134)

**AOLFR73 sequences:**

MNHVVKHNHTAVTKVTEFILMGITDNPGLQAPLFLGLIHYLVTVIGNLGMVILTYLDSKLHTP  
MYFFLRHLSITDLGYSTVIAPKMLVNFIVHKNTISYNWYATQLAFFEIFIISSELFILSAMAYDRYV  
AICKPLLYVIMAEKVLWVLVIVPYLYSTFVSLFTIKLFKLSFCGSNIISYFYCDCIPLMSILCSDT  
NELELILIFSGCNLLFSLSIVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVVIMFYGTLLFIYL  
55 QPKSSHTLAIDKMASVFYTLIPMLNPLIYSLRNKEVKDALKRTLNRFKIPI (SEQ ID NO: 135)

ATGAATCATGTGGTAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTCTCA  
 TGGGGATTACAGACAACCCTGGGCTGCAGGCTCCACTGTTTGGACTCTTCCTCATCATATA  
 TCTGGTCACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGCTA  
 CACACCCCCATGTACTTTTCCCTTAGACATTTGTCAATCACTGATCTTGGTTACTCCACTGT  
 5 CATTGCCCCGAAGATGTTAGTAACTTCATAGTGCACAAAAACACAATTTCTTACAATTGG  
 TATGCCACTCAGCTAGCATTCTTTGAGATTTTCATCATCTCTGAGCTCTTTATTCTATCAGC  
 AATGGCCTATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGTACGTGATCATCATGGCA  
 GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTCTATAGCACGTTTGTGTCACTATT  
 TCTCACAATTAAGTTATTTAAACTGCTTCTCTGTGGCTCAAACATAATCAGCTATTTTTACT  
 10 GTGACTGTATCCCTCTGATGTCCATACTCTGTTCTGACACAAATGAATTAGAATTAATAAT  
 TTTGATCTTCTCAGGCTGTAATTTGCTCTTCTCCCTCTCAATTGTTCTCATATCCTACATGTT  
 TATTCTAGTGGCCATTCTCAGAATGAACTCAAGGAAAGGGAGGTACAAAGCCTTCTCCACC  
 TGAGCTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTATTTATTTACTTGCA  
 ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTTATACCCTGTTG  
 15 ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAGATGCTCTAA  
 AGAGAACTTTAACCAATCGATTCAAATTTCCCATTTAA (SEQ ID NO: 136)

**AOLFR74 sequences:**

MEQHNLTTVNEFILTGITDIAELQAPLFALFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH  
 20 LAFMDLGYSTTVGPKMLVNFVVDKNIISYFCAATQLAFFLVFIGSELFILSAMSVDLYVAICNPL  
 LYTIVMSRRVCQVLVAIPYLYCTFISLLVTIKIFTLFCGYNVISHFYCDLPLPLLCNSNTHIELI  
 ILIFAADLISSLLIVLLSYLLILVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLLFMVYQPKSSH  
 SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLCNIFV (SEQ ID NO: 137)  
 25 ATGGAACAACACAATCTAACAACGGTGAATGAATTCATTCTTACGGGAATCACAGATATC  
 GCTGAGCTGCAGGCACCATTAATTTGCATTGTTCTCATGATCTATGTGATCTCAGTGATGG  
 GCAATTTGGGCATGATTGTCCTACCAAGTTGGACTCCAGGTTGCAAACCCCTATGTACTT  
 TTTTCTCAGACATCTGGCTTTCATGGATCTTGGTTATTCAACAACGTGGGGACCCAAAATG  
 TTAGTAAATTTTGTGTGGATAAGAATATAATTTCTTATTATTTTGTGCAACACAGCTAGC  
 30 TTCTTTCTTGTGTTCAATTGGTAGTGAACCTTTTTATTCTCTCAGCCATGTCCTACGACCTCT  
 ATGTGGCCATCTGTAACCCCTCTGCTATACACAGTAATCATGTACGAAGGGTATGTCAGGT  
 GCTGGTAGCAATCCCTTACCTCTATTGCACATTCATTTCTCTTCTAGTCACCATAAAGATTT  
 TTACTTTATCCTTCTGTGGCTACAACGTCATTAGTCATTTCTACTGTGACAGTCTCCCTTTG  
 TTACCTTTGCTTTGTTCAAATACACATGAAATTGAATTGATAATTCTGATCTTTGCAGCTAT  
 35 TGATTTGATTTCTCTCTCTGATAGTTCTTTTATCTTACCTGCTCATCCTTGTAGCCATTCT  
 CAGGATGAATTCGTGCTGGCAGACAAAAGGCTTTTTTCTACCTGTGGAGCCACCTGACAGTG  
 GTCATAGTGTCTATGGGACTTTGCTTTTCATGTACGTGCAGCCCAAGTCCAGTCATTCCTT  
 TGACACTGATAAAGTGGCTTCCATATTTTACACCCTGGTTATCCCCATGTTGAATCCCTTGA  
 TCTATAGTTTACGAAACAAAGATGTAATAATATGCCCTACGAAGGACATGGAATAACTTATG  
 40 TAATATTTTTGTTTAA (SEQ ID NO: 138)

**AOLFR75 sequences:**

MEGKNQTNISEFLLLGFSSWQQQVLLFALFLCLYLTGLFGNLLILLAIGSDHCLHTPMYFFLA  
 NLSLVDLCLPSATVPKMLLNQQTQTISYPGCLAQMYFCMMFANMDNFLTVMAYDRYVAI  
 45 CHPLHYSTIMALRLCASLVAAPWVIAILNPLLHTLMM AHLHFCSDNVIHHFFCDINSLLPLSCSD  
 TSLNQLSVLATVGLIFVPSVCILVSYILIVSAVMKVPSAQGKLKAFSTCGSHLALVILFYGANT  
 GVYMSPLSNHSTEKDSAASVIFMVVAPVLNPFYISLRNNELKGTLLKTLRPGAVAHACNPSTL  
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)  
 50 ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTTCTCCTCCTGGGCTTCTCAAGTTGGC  
 AACAACAGCAGGTGCTACTCTTTGCACTTTTCTGTGTCTCTATTTAACAGGGGCTGTTTGA  
 AACTTACTCATCTTGCTGGCCATTGGCTCGGATCACTGCCTTCACACACCCATGTATTTCTT  
 CCTTGCCAATCTGTCCTTGGTAGACCTCTGCCTTCCCTCAGCCACAGTCCCCAAGATGCTAC  
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCCTGGCTCAGATGTATTT  
 55 CTGTATGATGTTTGCCAATATGGACAATTTTCTTCTCACAGTGATGGCATATGACCGTTAC  
 GTGGCCATCTGTCACCCCTTACATTACTCCACCATTATGGCCCTGCGCCTCTGTGCCTCTCT

GGTAGCTGCACCTTGGGTCATTGCCATTTTGAACCCTCTCTTGCACACTCTTATGATGGCCC  
 ATCTGCACTTCTGCTCTGATAATGTTATCCACCATTTCCTTCTGTGATATCAACTCTCTCCTC  
 CCTCTGTCTGTTCCGACACCAGTCTTAATCAGTTGAGTGTCTGGCTACGGTGGGGCTGA  
 TCTTTGTGGTACCTTCAGTGTGTATCCTGGTATCCTATATCCTCATTGTTTCTGCTGTGATG  
 5 AAAGTCCCTTCTGCCCAAGGAAAACCAAGGCTTCTCTACCTGTGGATCTCACCTTGCCTT  
 GGTCATTCTTTTCTATGGAGCAACACAGGGGTCTATATGAGCCCTTATCCAATCACTCT  
 ACTGAAAAAGACTCAGCCGCATCAGTCATTTTATGGTTGTAGCACCTGTGTTGAATCCAT  
 TCATTTACAGTTTAAGAAACAATGAACTGAAGGGGACTTTAAAAAAGACCCTAAGCCGGC  
 CGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGGTGGATCA  
 10 TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)

**AOLFR76 sequences:**

MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLITLTGNLGMILLLDSHLHTPMYFFLSNLSLA  
 GIGYSSAVTPKVLTLGLLIEDKAISYSACAAQMFFCAVFATVENYLLSSMAYDRYAAVCNPLHY  
 15 TTTMTTRVCACLAIGCYVIGFLNASIQIGDTFRLSFCMSNVIIHFFCDKPAVITLTCSEKHISELIL  
 VLISFNVFFALLVTLISYLFILITILKRHTGKGYQKPLSTCGSHLIAIFLYITVIIMYIRPSSSHSM  
 DTDKIASVFTMIIPMLSPIVYTLRNKDVKNAFMKVVEKAKYSLDSVF (SEQ ID NO: 141)

ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCCAGAA  
 20 CTACAGGTTCCCTCTTTATCATGTTTACCCTCATCTACCTCATCACTCTGACTGGGAACCT  
 GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTTTCTCA  
 GTAACCTGTCTCTTGCAGGCATTGGTTACTCCTCAGCTGTCACTCCAAAGGTTTAACTGG  
 GTTGCTTATAGAAGACAAAGCCATCTCCTACAGTGCCTGTGCTGCTCAGATGTTCTTTGT  
 GCAGTCTTTGCCACTGTGAAAATTACCTCTTGTCTCAATGGCCTATGACCGCTACGCAG  
 25 CAGTGTGTAACCCCTACATTATACCACCACCATGACAACACGTGTGTGTGCTTGTCTGGC  
 TATAGGCTGTTATGTCATTGGTTTTCTGAATGCTTCTATCCAAATTGGAGATACATTTGCGC  
 TCTCTTTCTGCATGTCCAATGTGATTCATCACTTTTTCTGTGACAAACCAGCAGTCATTACT  
 CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTTGTTCCTATATCAAGTTTAAATGT  
 CTTTTTGCACCTCTTGTACCTTGATTTCTATCTGTTTCATATTGATCACCATTCTTAAGAG  
 30 GCACACAGGTAAGGGATACCAGAAAGCCTTATCTACCTGTGGTTCTCACCTCATTGCCATT  
 TTCTTATTTTATATAACTGTCATCATCATGTACATACGACCAAGTTCAGTCATTCCATGGA  
 CACAGACAAAATTGCATCTGTGTTCTACACTATGATCATCCCCATGCTCAGTCCTATAGTCT  
 ATACCCTGAGGAACAAAGACGTGAAGAATGCATTTCATGAAGGTTGTTGAGAAGGCAAAAT  
 ATTCTCTAGATTCACTCTTTAA (SEQ ID NO: 142)

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**AOLFR77 sequences:**

MGDVNQSVASDFILVGLFSHSGSRQLLFSLVAVMFVIGLLGNTVLLFLIRVDSRLHTPMYFLLS  
 QLSLFDIGCPMVTIPKMASDFLRGEGATS YGGGAAQIFFLTLMGVAEGVLLVLMSYDRYVAVC  
 QPLQYPVLMRRQVCLLMMGSSWVVGVLNASIQTSITLHFPYCASRIVDHFFCEVPALLKLSCA  
 40 DTCAYEMALSTSGVLILMLPLSLIATSYGHVLQAVLSMRSEEARHKAVTTCSSHITVVGFLFYGA  
 AVFMYMVPCAYHSPQQDNVVSFLYSLVPTLNPLIYSLRNPEVWMALVKVLSRAGLRQMC  
 (SEQ ID NO: 143)

ATGGGGGATGTGAATCAGTCGGTGGCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACT  
 45 CAGGATCACGCCAGCTCCTCTTCTCCCTGGTGGCTGTCATGTTTGTGATAGGCCTTCTGGGC  
 AACACCGTTCTTCTTCTTGTATCCGTGTGGACTCCCGGCTCCACACACCCATGTACTTCT  
 GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCACCATCCCCAAGATGGCA  
 TCAGACTTTCTGCGGGGAGAAGGTGCCACCTCCTATGGAGGTGGTGCAGCTCAAATATTCT  
 TCCTCACACTGATGGGTGTGGCTGAGGGCGTCTGTTGGTCTCATGTCTTATGACCGTTA  
 50 TGTGTGCTGTGTGCCAGCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGCTG  
 ATGATGGGCTCCTCCTGGGTGGTAGGTGTGCTCAACGCCTCCATCCAGACCTCCATCACCC  
 TGCATTTTCCCTACTGTGCCTCCCGTATTGTGGATCACTTCTTCTGTGAGGTGCCAGCCCTA  
 CTGAAGCTCTCCTGTGCAGATACCTGTGCCTACGAGATGGCGCTGTCCACCTCAGGGGTGC  
 TGATCCTAATGCTCCCTCTTCCCTCATCGCCACCTCCTACGGCCACGTGTTGCAGGCTGTT  
 55 CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGCTGTCAACACCTGCTCCTCGCACATCA  
 CGGTAGTGGGGCTCTTTTATGGTGCCGCCGTGTTTCATGTACATGGTGCCTTGCGCCTACCA

CAGTCCACAGCAGGATAACGTGGTTTCCCTCTTCTATAGCCTTGTCACCCCTACACTCAAC  
CCCCTTATCTACAGTCTGAGGAATCCGGAGGTGTGGATGGCTTGGTCAAAGTGCTTAGCA  
GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

5 **AOLFR78 sequences:**

MSPDGNHSSDPTEFVLAGLPNLNSARVELFSVFLVYLLNLTGNVLIVGVVRADTRLQTPMYF  
FLGNLSCLEILLTSVIIPKMLSNFLSRQHTISFAACITQFYFYFFLGASEFLLAVMSADRYLAICH  
PLRYPLLMGAVCFRVALACWVGGVLPVLGPTVAVALLPFCKQGA VVQHFFCDSGPLLRLAC  
TNTKKLEETDFVLASLVIVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVVTLFYGSAI  
10 FLYVRPSQSGSVDTNWAVTVITTFVTPLLNPFYALRNEQVKEALKDMFRKVAVGLGNLLLD  
KCLSEKAVK (SEQ ID NO: 145)

ATGAGTCCTGATGGGAACCACAGTAGTGATCCAACAGAGTTCGTCCTGGCAGGGCTCCCA  
AATCTCAACAGCGCAAGAGTGGAATTATTTCTGTGTTTCTTCTGTCTATCTCCTGAATCT  
15 GACAGGCAATGTGTTGATTGTGGGGGTGGTAAGGGCTGATACTCGACTACAGACCCCTAT  
GTACTTCTTTCTGGGTAACCTGTCCTGCCTAGAGATACTGCTCACTTCTGTCATCATTCCAA  
AGATGCTGAGCAATTTCTCTCAAGGCAACACACTATTTCTTTGCTGCATGTATCACCCA  
ATTCTATTTCTACTTCTTTCTCGGGGCTCCGAGTTCTTACTGTTGGCTGTCATGTCTGCGG  
ATCGCTACCTGGCCATCTGTCATCCTCTGCGCTACCCCTTGCTCATGAGTGGGGCTGTGTG  
20 CTTTCGTGTGGCCTTGGCCTGCTGGGTGGGGGACTCGTCCCTGTGCTTGGTCCCACAGTG  
GCTGTGGCCTTGCTTCTTTCTGTAAGCAGGGTGTGTGGTACAGCACTTCTTCTGCGACA  
GTGGCCCACTGCTCCGCTGGCTTGACCAACACCAAGAAGCTGGAGGAGACTGACTTTGT  
CCTGGCCTCCCTCGTCATTGTATCTTCTTGCTGATCACTGCTGTGTCTACGGCCTCATTG  
TGCTGGCAGTCCTGAGCATCCCCCTCTGCTTCAGGCCGTCAGAAGGCCCTTCTCTACCTGTAC  
25 CTCCCACCTTGATAGTGGTGACCCTCTTCTATGGAAGTGCCATTTTCTCTATGTGCGGCCAT  
CGCAGAGTGGTTCTGTGGACACTAAGTGGCAGTGACAGTAATAACGACATTTGTGACAC  
CACTGTTGAATCCATTCTATGCCTTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA  
CATGTTTAGGAAGGTAGTGGCAGGCGTTTATAGGAATCTTTACTTGATAAATGTCTCAGT  
GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

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**AOLFR79 sequences:**

MTPGELALASGNHTPVTKFILQGFSNYPDLQELLFGAILLIYAITVVGNLGMMLIFTDSHLQSP  
MYFFNLVLSFLDICYSVVTPKLLVNFLVSDKSISFEGCVVQLAFFVVHVTAESFLLASMAFYDR  
FLAICQPLHYGSIMTRGTCLQLVAVSYAFGGANSIAQTGNVFALPFCGPNQLTHYYCDIPLLH  
35 LACANTATARVVLVVSALVTLLPAAVILTSYCLVLVAIGRMRSVAGREKDLSTCASHFLAIAI  
FYGTVVFTYVQPHGSTNNTNGQVVSFYTIIIPMLNPFYSLRNKEVKALQRKLQVNIFFG  
(SEQ ID NO: 147)

ATGACACCTGGAGAACTAGCCCTTGCCAGTGGCAACCACACCCAGTCACCAAGTTCATCT  
40 TGCAGGGATTCTCCAATTATCCAGACCTCCAGGAGCTTCTCTTCGGAGCCATCCTGCTCAT  
CTATGCCATAACAGTGGTGGGCAACTTGGGAATGATGGCACTCATCTTCACAGACTCCCAT  
CTCCAAAGCCCAATGTATTTCTTCTCAATGTCCTCTCGTTTCTTGATATTTGTTACTCTTCT  
GTGGTCAACCTAAGCTCTTGGTCAACTTCTGGTCTCTGACAAGTCCATCTCTTTTGAGG  
GCTGTGTGGTCCAGCTCGCCTTCTTTGTAGTGCATGTGACAGCTGAGAGCTTCTGCTGGC  
45 CTCCATGGCCTATGACCGCTTCTAGCCATCTGTCAACCCCTCCATTATGGTTCTATCATGA  
CCAGGGGGACCTGTCTCCAGCTGGTAGCTGTGTCTATGCATTGGTGGAGCCAACTCCGC  
TATCCAGACTGGAAATGTCTTTGCCCTGCCTTTCTGTGGGGCCCAACCACTAACACACTAC  
TACTGTGACATAACACCCCTTCTCCACCTGGCTTGTGCCAACACAGCCACAGCAAGAGTGG  
TCCTCTATGTCTTTTCTGCTCTGGTCAACCTTCTGCCTGCTGCAGTCATTCTCACCTCCTACT  
50 GCTTGGTCTTGGTGGCCATTGGGAGGATGCGCTCAGTAGCAGGGAGGGAGAAGGACCTCT  
CCACTGTGCTCCCACTTTCTGGCCATTGCCATTTTCTATGGCACTGTGGTTTTCACCTAT  
GTTCAGCCCCATGGATCTACTAACAATACCAATGGCCAAGTAGTGTCCGTCTTCTACACCA  
TCATAATTCCCATGCTCAATCCCTTCATCTATAGCCTCCGCAACAAGGAGGTGAAGGGCGC  
TCTGCAGAGGAAGCTTCAGGTCAACATCTTTCCCGGCTGA (SEQ ID NO: 148)

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**AOLFR80 sequences:**

MEGINKTAKMQFFRPFSPDPEVQMLIFVVFLMMYLTSLGGNATIAVIVQINHSLHTPMYFFLA  
NLAVLEIFYTSSITPLALANLLSMGKTPVSITGCGTQMFFFVFLGGADCVLLVVMAYDRFIAICH  
PLRYRLIMSWSLCVELLVGSVLGFLLSLPLTILFHLFPCHNDEIYHFYCDMPAVMRLACADTR  
5 VHKTALYIISFIVLSIPLSLISISYVFIVVAILRIRSAEGRQQAYSTCSSHILVLLQYGCTSFYILSPS  
SSYSPEMGRVVSVAYTFTIPILNPLIYSLRNKELKDALRKALRKF (SEQ ID NO: 149)

ATGGAAGGAATAAAATAAACTGCAAAGATGCAGTTTTTCTTTTCGTCCATTCTCACCTGACC  
CTGAGGTCCAGATGCTGATTTTTGTGGTCTTCTGATGATGTATCTGACCAGCCTCGGTGG  
10 AAATGCTACAATTGCAGTCATTGTTTCAGATCAATCATTCCCTCCACACCCCATGTACTTTT  
TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCCATCACCCCATGGCCTTG  
GCAAACCTCCTTTCAATGGGCAAACTCCTGTTTCCATCACGGGATGTGGCACCCAGATGT  
TTTTCTTTGTCTTCTTGGGTGGGGCTGATTGTGTCTGCTGGTAGTCATGGCTTATGACCGG  
TTTATAGCGATCTGTACCCCTCTGCGATACAGGCTCATCATGAGCTGGTCCTTGTGTGTGG  
15 AGCTGCTGGTAGGCTCCTTGGTGTCTGGGGTCTGTTGTCACTGCCACTCACCATTTAATC  
TTCCATCTCCCATCTGCCACAATGATGAGATCTACCACTTCTACTGTGACATGCCTGCAGT  
CATGCGCCTGGCTTGTGCAGACACACGCGTTCACAAGACTGCTCTGTATATCATCAGCTTC  
ATCGTCTTAGCATCCCCCTCTCATTGATCTCCATCTCCTATGTCTTCATCGTGGTAGCCAT  
TTTACGGATCCGGTCAGCAGAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC  
20 TTAGTGGTCTCCTGTCAGTATGGCTGCACCAGCTTTATATACTTGTCCCCCAGTTCAGCTA  
CTCTCCTGAGATGGGCGGGTGGTATCTGTGGCCTACACATTTATCACTCCCATTTTAAAC  
CCCTTGATCTATAGTTTGAGGAACAAGGAACTGAAAGATGCCCTAAGGAAAGCATTGAGA  
AAATTCTAG (SEQ ID NO: 150)

**AOLFR81 sequences:**

MGVKNHSTVTEFLLSGLTEQAEQLPLFCLFLGIYTVTVVGNLSMISIRLNRLHTPMYYFLSS  
LSFLDFCYSSVITPKMMKLWMESHLPETRPSPRMMSNQTLVTEFILQGFSEHPEYRVFLFSCF  
LFLYSGALTGNVLITLAITFNPGLHAPMYFFLLNLATMDIICTSSIMPKALASLVSEESSISYGGC  
MAQLYFLTWAASSELLLLTVMAYDRYAACHPLHYSSMMSKVFCGLATAVWLLCAVNTAIH  
30 TGLMLRLDFCGPNVHHFFCEVPPLLLSCSSTYVNGVMIVLADAFYGIVNFLTIASYGFIVSSI  
LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL  
IYTLRNKEVKAALRLKLPFFRN (SEQ ID NO: 151)

ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCCAGAAACCCGTCCCAGCCCAAGGATG  
35 ATGAGTAACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTCGGAGCACCCAGAAT  
ACCGGGTGTCTTATTACAGCTGTTTCTCTTCTCTACTCTGGGGCCCTCACAGGTAATGTC  
CTCATCACCTTGGCCATCACGTTCAACCCTGGGCTCCACGCTCCTATGTACTTTTTCTTACT  
CAACTTGGCTACTATGGACATTATCTGCACCTCTTCCATCATGCCCAAGGCGCTGGCCAGT  
CTGGTGTGCGGAAGAGAGCTCCATCTCCTACGGGGGCTGCATGGCCAGCTCTATTTCTCA  
40 CGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTCATGGCCTATGACCGGTACGCAGC  
CATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC  
ACAGCCGTGTGGCTGCTCTGCGCGTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT  
TGGATTTCTGTGGCCCCAATGTCATTATCCATTTCTTCTGCGAGGTCCCTCCCTGCTGCTT  
CTCTCCTGCAGCTCCACCTACGTCAACGGTGTGATGATTGTCCTGGCGGATGCTTTCTACG  
45 GCATAGTGAACCTTCTGATGACCATCGCGTCTATGGCTTCATCGTCTCCAGCATCTGAA  
GGTGAAGACTGCCTGGGGGAGGCAGAAAGCCTTCTCCACCTGCTCTTCCACCTCACCGTG  
GTGTGCATGTATTACACCGCTGTCTTCTACGCCTACATAAGCCCGGTCTCTGGCTACAGCG  
CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACTGTGCTGAGTCTACCTCAACCCCT  
CATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTTCCCTTTCTTC  
50 AGAAATTA (SEQ ID NO: 152)

**AOLFR82 sequences:**

MQLNNNVTEFILLGLTQDPFWKKIVFVIFLRLYLGTLLGNLLIISVKASQALKNPMFFFLFYLSL  
SDTCLSTSIAPRMIVDALKKTTISFSECMIQVFSSHVFGCLEIFILILTAVDRYVDICKPLHYMTII  
55 SQWVCGLMAVAWVGSCVHSLVQIFLALSLPFCGPNVINHCFCDLQPLLKQACSETYVVNLLL

VSNSGAICAVSYVMLIFSIVFLHSLRNHSAEVIKKALSTCVSHIIVVILFFGPCIFMYTCPATVFP  
MDKMIAVFYTVGTSFLNPVIYTLKNTEVKSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

5 ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGGATTGACACAGGATCCTTTTT  
GGAAGAAAATAGTGTGTTTATTTTTTTCGCTCTCTACTTGGGAACACTGTTGGGTAATTT  
GCTAATCATTATTAGTGTCAAGGCCAGCCAGGCACCTAAGAACCCAATGTTCTTCTTCCTT  
TTCTACTTATCTTTATCTGATACTTGCCTCTCTACTTCCATAGCCCCTAGAATGATTGTGGA  
TGCCCTTTTGAAGAAGACAACCTATCTCCTTCAGCGAGTGCATGATCCAAGTCTTTTCATCC  
10 CATGTCTTTGGCTGCCTGGAGATCTTCATCCTCATCTCACGGCTGTTGACCGCTATGTGGA  
CATCTGTAAGCCCCTGCACTACATGACCATCATAAGCCAGTGGGTCTGTGGTGTGTTTGATG  
GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAGATTTTTCTTGCCCTGAGTTT  
GCCATTCTGTGGCCCCAATGTGATCAATCACTGTTTCTGTGACTTGACGCCCTTGTGAAA  
CAAGCCTGTTGAGAAACCTATGTGGTTAACTACTCCTGGTTTCCAATAGTGGGGCCATTT  
GTGCACTGAGTTATGTGCTAATATTCTCCTATGTCATCTTCTTGCACTTCTTGAGAAAC  
15 CACAGTGTGAGTGATAAAGAAAGCACTTCCACATGTGTCTCCACATCATTGTGGTCA  
TCTGTCTTTGGACCTTGCATATTTATGTACACATGCCCTGCAACCGTATTCCCCATGGAT  
AAGATGATAGCTGTATTTATACAGTTGGAACATCTTTTCTCAACCCTGTGATTTACACGCT  
GAAGAATACAGAAGTGAAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATTGATCACAGA  
TGACAAAAGATAA (SEQ ID NO: 154)

20

**AOLFR83 sequences:**

MGNWTAAVTEFVLLGFSLSREVELLLLVLPLTFLLLTLLGNLLIISTVLSCSRLHTPMYFFLCNL  
SILDILFTSVISPKVLANLGSRDKTISFAGCITQCYFYFFLGTVEFLLLTVMYSDRYATICPLRYT  
TIMRPSVCIGTVVFSWVGGFLSVLFPTILISQLPFCGSNIINHFFCDSGPLLALACADTTAIELMDF  
25 MLSSMVLCCIVLVAYSITYIILTIVRIPSASGRKKAFNTCASHLTIVIIPSGITVFIYVTPSQKEYL  
EINKIPLVLSSVTPFLNPFITYTLRNDTVQGVLRDVWVRVGVFEKRMRAVLRSLSSNKDHQ  
GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

30 ATGGGTAACTGGACTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCCTGAGCAGGG  
AGGTGGAGCTGCTGCTCCTGGTGCTCCTGCTGCCACGTTCTGCTGACTCTTCTGGGGAA  
CCTGCTCATCATCTCCACTGTGCTGTCTGCTCCCGCCTCCACACCCCCATGTACTTCTTCT  
TGTGCAACCTCTCTATCCTGGACATCCTCTTCACCTCAGTCATCTCTCAAAAAGTGTGGCC  
AACTTAGGATCTAGGGATAAAACCATCTCCTTTGCCGGATGTATCACCCAGTGCTATTTCT  
ACTTTTTCTTGGGCACAGTTGAGTTCCTCCTGCTGACGGTCATGTCCTATGACCGTTATGCC  
35 ACCATCTGCTGCCCCCTGCGGTACACCACCATCATGAGACCTTCTGTCTGCATTGGGACCG  
TTGTATTCTCTTGGGTGGGAGGCTTCCTGTCTGTGCTCTTTCCAACCATCCTCATCTCCCAG  
CTGCCCTTCTGTGGCTCCAATATCATTAAACCACTTCTTCTGTGACAGTGGACCTTGTGGC  
CCTGGCCTGTGCAGACACCACTGCCATCGAGCTGATGGATTTTATGCTTTCTTCCATGGTC  
ATCCTCTGTGTCATAGTCTCGTGGCCTATTCTATACGTACATCATCTTGACCATAGTGGC  
40 CATTCCTTCTGCAAGTGGAAGGAAGGCCTTTAATACCTGTGCTTCCACCTGACCATA  
GTCATCATTCCTAGTGGCATCACTGTGTTTATCTATGTGACTCCCTCCCAGAAAGAATATCT  
GGAGATCAACAAGATCCCTTTGGTTCTGAGCAGTGTGGTGAATTCCTCAACCCCTTT  
ATATATACTCTGAGGAATGACACAGTGCAGGGAGTCTCAGGGATGTGTGGGTGAGGGTT  
CGAGGAGTTTTTGAAAAGAGGATGAGGGCAGTGTGAGAAGCAGATTATCCTCCAACAAA  
45 GACCACCAAGGAAGGGCTTGCTCTTCTCCACCATGTGTCTATTCTGTAAAGCTCCAGTGT  
AG (SEQ ID NO: 156)

**AOLFR85 sequences:**

50 MGAKNNVTEFVFLFGLFESREMQHTCFVVFFLFHVLTVLGNLLVIITINARKTLKSPMYFFLSQL  
SFADICYPSTTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY  
TAIMDCRKCGLLAGASWLAGFLHSILQTLTQVLPFCGPNEIDNFFCDVHPLLKLACADTYMV  
GLIVVANSGMISLASFFILIISYVILLNLRSSQSEDRRKAVSTCGSHVITVLLVLMPPMFMYIRPS  
TTLAADKLIILFNIVMPPLLNLPIYTLRNDVKNAMRKLFRVKRSLGEK (SEQ ID NO: 157)

55 ATGGGTGCCAAGAACAATGTGACTGAGTTTGTGTTTTATTTGGCCTTTTTGAGAGCAGAGAGA  
TGCAGCATACATGCTTTGTGGTATTCTTCTCTTTTCATGTGCTCACTGTCCTGGGGAACCTT

CTGGTCATCATCACCATCAATGCTAGAAAGACCCTGAAGTCTCCCATGTATTTCTTCCTGA  
GCCAGTTGTCTTTTGCTGACATATGTTATCCATCCACTACCATAACCAAGATGATTGCTGAC  
ACTTTTGTGGAGCATAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTTCTGCCCA  
CTTCTTTGGTGGCACTGAGATCTTCTCCTTACAGCCATGGCCTATGACCGCTATGTGGCC  
5 ATCTGTAGGCCCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG  
GGGCTCCTGGTTAGCTGGCTTCTGCAATCCATCCTGCAGACCCCTCCTCACGGTTCAGCTG  
CCTTTTGTGGGCCCAATGAGATAGACAACCTTCTTCTGTGATGTTTCATCCCTGCTCAAGTT  
GGCCTGTGCAGACACCTACATGGTAGGTCATCGTGGTGGCCAACAGCGGTATGATTTCT  
Ttagcatcctttttatccttatcatttccatatgttatcatcttactgaacctaaagaagcca  
10 GTCATCTGAGGACCGCGTAAGGCTGTCTCCACATGTGGCTCACACGTAATCACTGTCCTT  
TTGGTTCTCATGCCCCCATGTTTCATGTACATTCGTCCCTCCACCACCCTGGCTGCTGACAA  
ACTTATCATCCTCTTTAACATTGTGATGCCACCTTTGCTGAACCCCTTGATCTATACTAA  
GGAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG  
AGAAGTGA (SEQ ID NO: 158)

15

**AOLFR86 sequences:**

MQLVLLLMFLVFIGNTAPAFSVTLESMDIPQNITEFFMLGLSQNSEVQRVLFVVFLLIYVVTVC  
GNMLIVVTITSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFGAHP  
LGGVEILLTVMAYDRYVAICKPLHNTTIMTRHLCAMLVGVAWLGGFLHSLVQLLLVLWLPFC  
20 GPNVINHFACDLYPLLEVACTNTYVIGLLVVANSGLICLLNFLMLAASYIVILYSLRSHSADGRC  
KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMR  
KLFTW (SEQ ID NO: 159)

ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT  
25 CTCAGTGACCTTGAATCTATGGACATACCACAAAATATCACAGAATTTTTCATGCTGGGG  
CTCTCACAGAACTCAGAGGTACAGAGAGTTCTCTTTGTGGTCTTTTGTGCTGATCTATGTGG  
TCACGGTTTGTGGCAACATGCTCATTGTGGTCACTATCACCTCCAGCCCCACGCTGGCTTC  
CCCTGTGATTTTTCTGGCCAACCTATCCTTTATTGACACCTTTTATTCTTCTTCTATGGC  
TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGCTGCATG  
30 GCTCAGCTCTTTGGAGCTCATTTTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG  
CTTATGACCGCTATGTGGCCATCTGTAAGCCCTGCACAATACTACCATCATGACCAGGCA  
TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGGCTTCTGCAATTCATTGGTTTCA  
CTCCTCCTGGTCTTTGGTTGCCCTTCTGTGGGCCCAATGTGATCAATCACTTTGCCTGTGA  
CTTGTAACCTTTGCTGGAAGTTGCTGCACCAATACGTATGTCATTGGTCTGCTGGTGGTT  
35 GCCAACAGTGTTTAACTGCCTGTTGAACCTTCTCATGCTGGCTGCCTCCTACATTGTCAT  
CCTGTACTCCTTGAGGTCCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA  
GCCCACCTTCAATTGTTGTTGCCTTGTCTTTGTGCCCTGTATATTTACTTATGTGCATCCATTT  
TCTACTTTACCTATAGACAAAAATATGGCATTATTTTATGGTATTCTGACACCTATGTTGAA  
TCCACTCATTTATACCCTGAGAAATGAAGAGGTAAAAAATGCCATGAGAAAGCTCTTTACA  
40 TGGTAA (SEQ ID NO: 160)

**AOLFR87 sequences:**

MNNIAQLSLGFIDLIPSVLQKIILTKIILLFKMYVSNCPNCAIHRKINYPNTKLD FEQVNNITEFI  
LLGLTQNAEAQKLLFAVFTLIYFLTMVDNLIIVVTITSPALDSPVYFFLSFFSFIDGCSSTMAP  
45 KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEIILLVVMAYDCYVAICKPLYLITMNRQVCG  
LVAMAWVGGFLHALIQMLLIVWLPFCGPNVIDHFICDLFLLKLSCDTHVFLFVAANSGLM  
CMLJFSILITSYVLILCSQRKALSTCAFHITVVVLFVPCILVYLRPMITFPIDKAVSVFYTVVTPM  
LNPLIYTLRNTTEVKNAMKQLWSQIIWGNLDCD (SEQ ID NO: 161)

ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTTAC  
AGAAAATAATCCTGACCAAAATTATTTTATTGTTCAAATGTATGTGTCAAATTGCAATCC  
TTGTGCTATTACAGAAAAATCAATTATCCAAATACCAAAGTGGATTCGAGCAAGTGAAC  
AACATAACGGAATTCATCTTGCTTGGCCTGACACAGAACGCAGAGGCACAGAACTCTTGT  
TTGCTGTGTTTACACTCATCTACTTTCTACCATGGTAGACAACCTAATCATTGTGGTGACA  
55 ATCACCACCAGCCCAGCCCTGGACTCCCCCGTATTTTTTCTGTCTTTCTTTCTTCTCAT  
AGATGGCTGCTCCTCTTCTACCATGGCCCCCAAAATGATATTTGACTTACTCACTGAAAAG

AAAACTATTTCTTCAGTGGGTGCATGACCCAGCTCTTTGTAGAACATTTCTTTGGGGGAG  
 TTGAGATCATTCTGCTCGTGGTGATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCCCT  
 GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCTCCTGGTGGCCATGGCATGGGTCT  
 5 GGGGGATTTCACGCTCTGATTCAAATGCTTTTAATAGTCTGGCTGCCCTTCTGTGGCCC  
 CAATGTCATTGACCATTTTCATCTGTGACCTTTCCCTCTGCTAAAACTCTCCTGCACTGACA  
 CTCACGTCTTTGGACTCTTTGTTGCCGCCAACAGTGGGCTGATGTGTATGCTCATTTTTTCT  
 ATTCTTATTACCTCTTACGTCCTAATCCTCTGCTCACAGCGGAAGGCTCTCTCTACCTGCGC  
 CTTCCATATCACTGTAGTCGTCCTATTCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA  
 10 TGATCACCTTCCCTATTGATAAAGCTGTGTCTGTGTTTTATACTGTGGTAACACCCATGTTA  
 AACCCTTTAATCTACACCCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG  
 AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

#### AOLFR88 sequences:

15 MWQKNQTSADFILEGLFDDSLTHLFLFSLTMVVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ  
 LSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYLCLGGAECFLAVMSYDRYVAICH  
 PLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHFPFCGPRKVYHFYCEFPVVKLV  
 GDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSKRNAFATCGSHLTVVSLWFGACIFS  
 YMRPRSQCILLQNKVGSVFSIHTPTLNSLIYTLRNKDVAKALRRVLRRDVITQCIQRLQLWLP  
 RV (SEQ ID NO: 163)

20 ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT  
 CCCTTACCCACCTTTTCCTTTCTCCTTGACCATGGTGGTCTTCCTTATTGCGGTGAGTGGC  
 AACACCCTCACCATTCTCCTCATCTGCATTGATCCCAGCTTCATACACCAATGTATTTCT  
 25 GCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAATCATCCTGAAGATGGCT  
 ACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTCC  
 TCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCATGTCCTATGACCGCTAT  
 GTTGCCATCTGTATCCACTGCGCTATGCTGTGCTCATGAACAAGAAGGTGGGACTGATGA  
 TGGCTGTCTGTATGTTGGGGGCATCCGTGAACCTCCCTAATTCACATGGCGATCTTGAT  
 30 GCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGAGTTCCAGCTGTTG  
 TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTACATCAGCAGCATTCT  
 CCTCCTCCTCCCATCTTCCTGATTTCTACATCCTATGTCTTCATCCTTCAAAGTGTCAATCA  
 GATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCTCCCACCTCACGGTG  
 GTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCTACATGAGACCCAGGTCCCAGTGCACCT  
 35 ATTCGAGAACAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCACATTGAATTTCTCTG  
 ATTTATACTCTCCGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGTGAGGAGAGAT  
 GTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCGAGTGTAG (SEQ ID NO:  
 164)

#### AOLFR89 sequences:

40 MLDPSSISHTLYLHSLFPQGLRKGMWQKNQTSADFILEGLFDDSLTHLFLFSLTMVVFLIAVS  
 GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYL  
 CLGGAECFLAVMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHF  
 PFCGPRKVYHFYCEFPVVKLVCGDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSK  
 RNAFATCGSHLTVVSLWFGACIFS YMRPRSQCILLQNKVGSVFSIHTPTLNSLIYTLRNKDVA  
 45 KALRRVLRRDVITQCIQRLQLWLP (SEQ ID NO: 165)

ATGCTGGACCCAGTATTTCCAGTCACACTCTTTATCTCCACTCTCTGTTTCCTCAGGGATT  
 GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGG  
 50 GCTCTTCGATGACTCCCTTACCCACCTTTTCCTTTCTCCTTGACCATGGTGGTCTTCCTTAT  
 TGCGGTGAGTGGCAACACCCTCACCATTCTCCTCATCTGCATTGATCCCAGCTTCATACA  
 CCAATGTATTTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT  
 CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA  
 ACCCAGCACTTCCCTCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCTATGTC  
 CTATGACCGCTATGTTGCCATCTGTCTCACTGCGCTATGCTGTGCTCATGAACAAGAAG  
 55 GTGGGACTGATGATGGCTGTCTATGTTGGGGGCATCCGTGAACCTCCCTAATTCACA  
 TGGCGATCTTGATGCACTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGA

GTTCCCAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC  
 ATCAGCAGCATTCTCCTCCTCCTCCCCATCTTCCTGATTTCTACATCCTATGTCTTCATCCTT  
 CAAAGTGTCAATTAGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCT  
 CCCACCTCACGGTGGTTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGG  
 5 TCCAGTGCACCTCTATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCA  
 CATTGAATTCTCTGATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT  
 GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTG  
 TAG (SEQ ID NO: 166)

10 **AOLFR90 sequences:**

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF  
 VLLGLSQNPVQEIFVVFVFLVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI  
 TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL  
 CGILMGVAWTGGLLHSMIQILFTFQLPFCGPNVINHFMCPLYLLELACTDTHIFGLMVVINS  
 15 FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA  
 AIFYIILNPLNPLYTFRNKEVKQAMRRIWNRMLMVVSDEKENIKL (SEQ ID NO: 167)

ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACCTTGGATGTACCAACTTGTTAA  
 TGACTATGATACCACAAAATTGATCTGAAGCAAATTTTCCTTTGTCCTAATTGCAGACTATA  
 20 CATGATCCCTGTTGGAGCTTTCATCTTTTCCTTGGGAAACATGCAAAACCAAAGCTTTGTA  
 ACTGAGTTTGTCTCCTGAGACTTTCACAGAATCCAAATGTTTCAGGAAATAGTATTTGTTG  
 TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATCTC  
 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGTCCTTCTGGA  
 TCGTGTCTTCTCATCTGTCTATCACCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA  
 25 ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG  
 AGGTGATTGTCCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA  
 TTAATCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG  
 GGCCTCTTGCAATCCATGATACAAATCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA  
 TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC  
 30 ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG  
 TTGCTTGTCTCCTATGCTGTCTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG  
 GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA  
 TATTTGTATATACACGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT  
 ATCATCTTAAATCCCTTGTCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC  
 35 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA  
 AACTTTAA (SEQ ID NO: 168)

**AOLFR91 sequences:**

MGNWSTVTEITLIAFPALLEIRISLFVVLVVYTLTATGNITHSLIWIHRLQTPMYFFLSNLSFL  
 40 DILYTTVITPKLLACLGEKTIISFAGCMIQTYFYFFLGTVEFILLAVMSFDRYMAICDPLHYTVI  
 MNSRACLILLVLCWVGAFSLVLFPTIVVTRLPHYCRKEINHFFCDIAPLLQVACINTHLIEKINFL  
 SALVILSSLAFTTGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSLD  
 YDKVA AVLITVVTPLNPFYSLRNEKVQEVLRFTVNRIMTLIQRKT (SEQ ID NO: 169)

ATGGGAAACTGGAGCACTGTGACTGAAATCACCTAATTGCCTTCCCAGCTCTCCTGGAGA  
 TTCGAATATCTCTCTTCGTGGTTCTTGTGGTAACTTACACATTAACAGCAACAGGAAACAT  
 CACCATCATCTCCCTGATATGGATTGATCATCGCCTGCAAACTCCAATGTACTTCTCCTCA  
 GTAATTTGTCTTTCTGGATATCTTATACACCACTGTCATTACCCCAAAGTTGTTGGCCTGC  
 CTCCTAGGAGAAGAGAAAACCATATCTTTGCTGGTTGCATGATCCAAACATATTTCTACT  
 50 TCTTTCTGGGGACGGTGGAGTTTATCCTCTTGGCGGTGATGTCCTTTGACCGCTACATGGC  
 TATCTGCGACCACTGCACTACACGGTCATCATGAACAGCAGGGCCTGCCTTCTGCTGGTT  
 CTGGGATGCTGGGTGGGAGCCTTCTGTCTGTGTTGTTTCCAACCATTTGTAGTGACAAGGC  
 TACCTTACTGTAGGAAAGAAATTAATCATTTCTTCTGTGACATTGCCCTCTTCTCAGGTG  
 GCCTGTATAAATACTCACCTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTTGTATCCT  
 55 GAGCTCCCTGGCATTCACTACTGGGTCTACGTGTACATAATTTCTACCATCCTGCGTATCC  
 CCTCCACCCAGGGCCGTCAGAAAGCTTTTCTACCTGTGCTTCTCACATCACTGTTGTCTCC

ATTGCCCCACGGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAACTCCTCACTGGATT  
ATGACAAGGTGGCCGCTGTCCTCATCAGTGGTGACCCCTCTCCTGAACCCTTTTATCTA  
CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTTGAGAGAGACAGTGAACAGAATCATGAC  
CTTGATACAAAGGAAACTTGA (SEQ ID NO: 170)

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**AOLFR92 sequences:**

MRNGTVITEFILLGFPVIOGLQTPLFIAIFLTYILTLAGNGLIATVWAEPRLOIPMYFFLCNLSFLE  
IWYTTTTVIPKLLGTFVVARVICMSCLLQAFFHFFVGTTEFLILTIMSFDRLYTICNPLHHPTIM  
TSKLCLQLALSSWVVGFTIVFCQTMILLIQLPFCGNNVISHFYCDVGPLSKAACIDTSILELLGVIA  
TILVIPGSLLFNMISYIYILSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK  
INKVSVLNTILTPLLNPFIYTIRNKEVKALRKAMTCPKTGHAK (SEQ ID NO: 171)

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ATGAGAAATGGCACAGTAATCACAGAATTCATCCTGCTAGGCTTTCCTGTTATCCAAGGCC  
TACAAACACCTCTCTTTATTGCAATCTTCTCACCTACATATTAACCCTTGACAGGCAATGGG  
CTTATTATTGCCACTGTGTGGGCTGAGCCCAGGCTACAAATTCCAATGTACTTCTTCCTTTG  
TAACCTGTCTTTCTTAGAAATCTGGTACACCACCACAGTCATCCCCAACTGCTAGGAACC  
TTGTAGTGGCAAGAACAGTAATCTGCATGTCTGCTGCCTGCTGCAGGCCTTCTTCCACT  
TCTCGTGGGCACCACCGAGTTCCTTGATCCTCACTATCATGTCTTTTGACCGCTACCTCACC  
ATCTGCAATCCCCCTTACCACCCCCACCATCATGACCAGCAAACCTCTGCCTGCAGCTGGCCC  
TGAGCTCCTGGGTGGTGGGCTTCACCATTTGTCTTTTGTGACGATGTGCTCATCCAGTT  
GCCATTCTGTGGCAATAATGTTATCAGTCATTTCTACTGTGATGTTGGGCCAGTTTGAAA  
GCCGCTGCATAGACACCAGCATTTTGGAACTCCTGGGCGTCATAGCAACCATCCTTGTA  
TCCAGGGTCACTTCTCTTTAATATGATTTCTTATATCTACATTCTGTCCGCAATCCTACGA  
ATTCCTTCAGCCACTGGCCACCAAAAGACTTTCTCTACCTGTGCCTCGCACCTGACAGTTGT  
CTCCCTGCTCTACGGGGCTGTTCTGTTTCATGTACCTAAGACCCACAGCACACTCCTCCTTTA  
AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCCTCACCCCCCTTCTGAATCCCTTTATT  
TATACTATTAGAAACAAGGAGGTGAAGGGAGCCTTAAGAAAGGCAATGACTTGCCCAAAG  
ACTGGTCATGCAAAGTAA (SEQ ID NO: 172)

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**AOLFR93 sequences:**

MLMNYSSATEFYLLGFPGSEELHHILFAIFFFFYLVTLMGNTVIIMIVCVDKRLQSPMYFFLGHL  
SALEILVTIIVPVMWLWGLLPQMITYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN  
PLRYNIIMNRHTCNFVVLVSWVFGFLFQIWPVYVMFQLTYCKSNVNNFFCDRGQLKLSCN  
NTLFTEFILFLMAVFLVFLGSLIPTIVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCLFLY  
VKPKQTQAADYNWVVSMLMVSVVTPFLNPFIFTLRNDKVIEALRDGVKRCCLFRN (SEQ ID  
NO: 173)

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ATGTTGATGAATTACTCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA  
ACTACATCATATCCTTTTTGCTATATTCTTCTTTTCTACTTGGTGACATTAATGGGAAACA  
CAGTCATCATCATGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCCTC  
GGCCACCTCTCTGCCCTGGAGATCCTGGTCACAACCATAATCGTCCCCGTGATGCTTTGGG  
GATTGCTGCTCCCTGGGATGCAGACAATATATTGTCTGCCTGTGTTGTCCAGCTCTTCTTG  
TACCTTGCTGTGGGGACAACAGAGTTTCGCACTTGGAGCAATGGCTGTGGACCGTTATG  
TGGCTGTCTGTAACCCTCTGAGGTACAACATCATTATGAACAGACACACCTGCAACTTTGT  
GGTTCTTGTGTCTATGGGTGTTTGGGTTTCTTTTTCAAATCTGGCCGGTCTATGTCATGTTTC  
AGCTTACTTACTGCAAATCAAATGTGGTGAACAATTTTTTTGTGACCGAGGGCAATTGCT  
CAAACATCCTGCAATAATACTCTTTTCACGGAGTTTATCCTCTTCTTAATGGCTGTTTTTG  
TTCTCTTTGGTTCTTTGATCCCTACAATTGTCTCCAACGCCTACATCATCTCCACCATTCTC  
AAGATCCCGTCATCCTCTGGCCGGAGGAAATCCTTCTCCACTTGTGCCTCCCACTTCACCTG  
TGTTGTGATTGGCTACGGCAGCTGCTTGTCTCTACGTGAAACCAAGCAAACGCAGGCA  
GCTGATTACAATTGGGTAGTTTCCCTGATGGTTTCAGTAGTAACTCCTTCTCAATCCTTT  
CATCTTACCCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC  
TGTCAACTATTCAAGGAATTAG (SEQ ID NO: 174)

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**AOLFR94 sequences:**

METWVNQSYTDGFFLLGIFSHSTADLVLFSSVVMVFTVALCGNVLLIFLIYMDPHLHTPMYFF  
LSQLSLMDLMLVCTNVPKMAANFLSGRKSISFVCGCIQIGLVCLVSGEGLLLGLMAYDRYVA  
ISHPLHYPILMNQVRVCLQITGSSWAFGIIDGLIQMVVVMNFPYCGLRKVNHFFCEMLSLLKLAC  
5 VDTSLFEKVIFACCVFMLLFPFSIIVASYAHILGTVLQMHSAAWKKALATCSSHLTAVTLFYG  
AAMFIYLRPRHYRAPSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGLDRCRIGSQH  
(SEQ ID NO: 175)

10 ATGGAGACGTGGGTGAACCAAGTCTACACAGATGGCTTCTTCCTCTTAGGCATCTTCTCCC  
ACAGTACTGCTGACCTTGTCTCTTCTCCGTGGTTATGGCGGTCTTCACAGTGGCCCTCTGT  
GGGAATGTCCTCCTCATCTTCTCATCTACATGGACCCTCACCTTCACACCCCATGTACTT  
CTTCCTCAGCCAGCTCTCCCTCATGGACCTCATGTTGGTCTGTACCAATGTGCCAAAGATG  
GCAGCCAACTTCCTGTCTGGCAGGAAGTCCATCTCCTTTGTGGGCTGTGGCATACAAATTG  
GCCTCTTTGTCTGTCTTGTGGGATCTGAGGGGCTCTTGCTGGGACTCATGGCTTATGACCG  
15 CTATGTGGCCATTAGCCACCCACTTCACTATCCCATCCTCATGAATCAGAGGGTCTGTCTCC  
AGATTACTGGGAGCTCCTGGGCCCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT  
AATGAATTTCCCTACTGTGGCTTGAGGAAGGTGAACCATTTCTTCTGTGAGATGCTATCC  
TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAGAAGGTGATATTTGCTTGCTGTG  
TCTTCATGCTTCTCTTCCCATCTCCATCATCGTGGCCTCCTATGCTCACATTCTAGGGACT  
20 GTGCTGCAAATGCACTCTGCTCAGGCCTGGAAAAAGGCCCTGGCCACCTGCTCCTCCCACC  
TGACAGCTGTCACCCTCTTCTATGGGGCAGCCATGTTTATCTACCTGAGGCCTAGGCACTA  
CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGTCTTACTCCCATGCTC  
AACCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGGCACTGAGGAAGGGGCTG  
GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

25

**AOLFR95 sequences:**

MLGSKPRVHLIYLPASQQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILLFLLFLFVYAMILL  
GNVGMMTIIMTDPRLNTPMYFFLGNLSFIDLFYSSVIEPKAMINFWSENKSISFAGCVAQLFLFA  
LLIVTEGFLLAAMAYDRFIAICNPLLYSVQMSTRLCTQLVAGSYFCGCISSVIQTSMTFTLSFCAS  
30 RAVDHFYCDRPLQRLSCSDLFIHRMISFSLSCIILPHTIIVSYMYIVSTVLKIHSTEGHKKAFST  
CSSHLGVVSVLYGAVFFMYLTPDRFPELSKVASLCYSLVTPMLNPLIYSLRNKDVQEALKKFLE  
KKNIL (SEQ ID NO: 177)

35 ATGCTAGGATCCAAACCAAGAGTTCATTTGTATATTTTGCCCTGTGCCTCTCAACAGGTTTC  
TACCATGGGTGACAGGGGAACAAGCAATCACTCAGAAATGACTGACTTCATTCTTGCAGG  
CTTCAGGGTACGCCAGAGCTCCACATTCTCCTCTTCCTGCTATTTTGTGTTTATGCCA  
TGATCCTTCTAGGGAATGTTGGGATGATGACCATTATTATGACTGATCCTCGGCTGAACAC  
ACCAATGTATTTTTCCTAGGCAATCTCTCCTTCATTGATCTTTTCTATTCTGTTATTGA  
ACCCAAGGCTATGATCAACTTCTGGTCTGAAAACAAGTCTATCTCCTTTGCAGGCTGTGTG  
40 GCCCAGCTCTTTCTCTTTGCCCTCCTCATTGTGACTGAGGGATTTCTCCTGGCGGCCATGGC  
TTATGACCGCTTATTGCCATCTGCAACCCCTCTGCTCTACTCTGTTCAAATGTCCACACGTC  
TGTGTACTCAGTTGGTGGCTGGTTCCTATTTTGTGGCTGCATTAGCTCAGTTATTACAGACT  
AGCATGACATTTACTTTTATCTTTTTGCGCTTCTCGGGCTGTTGACCACTTTTACTGTGATTC  
TCGCCCCACTTCAGAGACTGTCTTGTCTGATCTCTTTATCCATAGAATGATATCTTTTTCCT  
45 TATCATGTATTATTATCTTGCCTACTATCATAGTCATTATAGTATCTTACATGTATATTGTG  
TCCACAGTTCTAAAGATACTTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT  
CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGTCTTTTTTATGTATCTCACTCCTGAC  
AGATTTTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTTGA  
ATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAATTTCTAGA  
50 GAAGAAAAATATTATTCTTTGA (SEQ ID NO: 178)

**AOLFR96 sequences:**

MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAIYTVTLLGNFLIVTVTSVDLALQTPMYFFLQN  
LSLLEVCFITLVMVPKMLVDLVSPRKISFVCGGTQMYFFFFFGSSECFLLSMMAAYDRFVAICNP  
55 LHYSVIMNRSCLWMAIGSWMSGVPVSMQLTAWMMALPFCGPNAVDFHFCDDGPPVLKLVTV  
DTTMYEMQALASTLLFIMFPFCLILVSYTRIITILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL

TYLRPKSNQSPESKKLVSLSYTVITPMLNPITYGLRNNEVKGAVKRTITQKVLQKLDVF (SEQ ID NO: 179)

5 ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATTCTTCTTGGTTTTACAAACAACC  
CCGAGATGCAAGTTTCCCTCTTTATTTTTTCTGGCCATTTATACAGTCACTTTGTTGGGC  
AACTTTCTTATTGTCACAGTTACCAGTGTGGATCTCGCACTTCAAACACCCATGTACTTCTT  
TCTTCAAATCTGTCACTTCTTGAAGTATGTTTACCTTGGTTATGGTGCCAAAAATGCTTG  
TAGATCTAGTGTCCCAAGGAAAATTATCTCTTTTGTGGGCTGTGGTACCCAGATGTACTT  
CTTCTTCTTCTTGGCAGTTCTGAATGTTTCTTCTCTCCATGATGGCTTATGATCGCTTGT  
10 GGCCATCTGTAACCCTCTCCATTATTCAGTCATAATGAACAGGTCCCTATGCTTGTGGATG  
GCCATAGGCTCTTGGATGTCCGGTGTTCCTGTGTCTATGCTACAGACAGCTTGGATGATGG  
CCCTTCTTTCTGTGGACCAAATGCCGTGGACCACTTTTCTGTGATGGTCCCCCAGTGTTA  
AAACTAGTCACAGTGGATAACAACCATGTATGAAATGCAAGCACTTGCTCCACACTCCTGT  
TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTACACCCGATTATCATAACAATTCTG  
15 AGGATGTCCTCTGCCACTGGCCGCCAGAAGGCATTTTCTACTTGTTCCTCACACCTCATTGT  
GGTGTCCCTCTTCTACGGAACAGCCAGTCTGACCTACCTGCGGCCCAAATCAAACCAGTCC  
CCTGAGAGCAAGAAGCTAGTGTCAATTGTCTACACTGTCATCACACCTATGCTAAACCCCA  
TCATCTACGGCCTGAGGAACAATGAAGTGAAAGGGGCTGTCAAGAGGACAATCACTCAAA  
AAGTCTTACAGAAGTTAGATGTGTTTTGA (SEQ ID NO: 180)

20

**AOLFR97 sequences:**

MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSMVVPFSIAEHWRMRMKGANLSQGMFEL  
LGLTTDPQLQRLLFVFLGMYTATLLGNLVMFLLHVSATLHTPMYSLKSLSFLDFCYSSTVV  
PQTLVNFLAKRKVISYFGCMTQMFFYAGFATSECYLIAAMAYDRYAAICNPLLYSTIMSPEVC  
25 ASLIVGSYSAGFLNSLIHTGCFSLKFCGAHVVTHFFCDGPPLSLSCVDTSLCEILLFIFAGFNLLS  
CTLTILISYFLILNTILKMSSAQGRFKAFSTCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRTVA  
VIYTVVIPVLNPLMYSLRNKDVKKALIKVWGRKTME (SEQ ID NO: 181)

30 ATGACAGAGTTTCATCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAGGCTGT  
CCTTAGGCAGAAATTAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTTATGGTGGTGCC  
TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAAACCTGAGCCAAGGGAT  
GGAGTTTGAGCTCTTGGGCCTCACCCTGACCCCACTCCAGAGGCTGCTCTTCGTGGTG  
TTCTGGGCATGTACACAGCCACTCTGCTGGGGAACCTGGTCATGTTCTCCTGATCCATG  
TGAGTGCCACCCTGCACACACCCATGTACTCCCTCCTGAAGAGCCTCTCCTTCTTGATTTC  
35 TGCTACTCCTCCACGGTTGTGCCCCAGACCCTGGTGAACCTCTTGCCAAAGAGGAAAGTGA  
TCTCTTATTTTGGCTGCATGACTCAGATGTTCTTCTATGCGGGTTTTGCCACCAGTGAGTGC  
TATCTCATCGCTGCCATGGCCTATGACCGCTATGCCGCTATTTGTAACCCCTGCTCTACTC  
AACCATCATGTCTCCTGAGGTCTGTGCCTCGCTGATTGTGGGCTCCTACAGTGCAGGATTC  
CTCAATTCTCTTATCCACACTGGCTGTATCTTTAGTCTGAAATTCTGCGGTGCTCATGTCTG  
40 CACTCACTTCTTCTGTGATGGGCCACCCATCTGCTTGTCTTGTGTAGACACCTCACTGT  
GTGAGATCCTGCTCTTCATTTTGTCTGGTTTCAACCTTTTGAGCTGCACCCTCACCATCTTG  
ATCTCCTACTTCTTAATTCTCAACACCATCCTGAAAATGAGCTCGGCCAGGGCAGGTTTA  
AGGCATTTTCCACCTGTGCATCCACCTCACTGCCATCTGCCTCTTCTTTGGCACAACACTT  
TTATGTACCTGCGCCCCAGGTCCAGCTACTCCTTGACCCAGGACCGCACAGTTGCTGTCA  
45 TCTACACAGTGGTGATCCAGTGCTGAACCCCTCATGTACTCTTTGAGAAACAAGGATGT  
GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)

**AOLFR98 sequences:**

MRGFNKTTVVTFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGLFI  
50 LSFSESCYTFVPIQLLVHLLSDTKTISFMACATQLFFFLGFACTNCLLIAVMGYDRYVAICHPLR  
YTILNKRLGLELISLGSATGFFIALVATNLICDMRFCGPNRVNHYFCDMAPVIKLACTDTHVKE  
LALFSLSILVIMVPFLILISYGFIVNTILKIPSAEGKKAFTVCASHLTVFVHYGCASIYLRPKSK  
SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)

55 ATGCGAGGTTTCAACAAAACCACTGTGGTTACACAGTTCATCCTGGTGGGTTTCTCCAGCC  
TGGGGGAGCTCCAGCTGCTGCTTTTGTCTCTTCTCTCTCTATACTTGACAATCCTGGTG



5   GCCAATGTGACCATCATGGCCGTTATTCGCTTCAGCTGGACTCTCCACACTCCCATGTATG  
 GCTTCTATTTCATCCTTTTCATTTTCTGAGTCCTGCTACACTTTTGTGCATCATCCCTCAGCTGC  
 TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTTCATGGCCTGTGCCACCCAGCTGTT  
 CTTTTTCCCTTGGCTTTGCTTGCACCAACTGCCTCCTCATTGCTGTGATGGGATATGATCGCT  
 10   ATGTAGCAATTTGTACCCCTCTGAGGTACACACTCATCATAAAACAAAAGGCTGGGGTTGGA  
 GTTGATTTCTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGGCCACCAACCTCATT  
 GTGACATGCGTTTTTGTGGCCCCAACAGGGTTAAACCACTATTTCTGTGACATGGCACCTGT  
 TATCAAGTTAGCCTGCACTGACACCCATGTGAAAGAGCTGGCTTTATTAGCCTCAGCATC  
 CTGGTAATTATGGTGCCTTTTCTGTTAATTCTCATATCCTATGGCTTCATAGTTAACACCAT  
 15   CCTGAAGATCCCCTCAGCTGAGGGCAAGAAGGCCTTTGTACCTGTGCCTCACATCTCACT  
 GTGGTCTTTGTCCACTATGGCTGTGCCTCTATCATCTATCTGCGGCCCAAGTCCAAGTCTGC  
 CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTTACTCCCTTACTTAATCCT  
 CTTGTCTACAGTCTGAGGAACAAAGAGGTA AAAA ACTGCATTGAAAAGAGTTCTTGAATG  
 CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

15

**AOLFR99 sequences:**

20   MERNVETVREVIFLGFSSLARLQQLLFVIFLLLYLFTLGTNAIIISTIVLDRALHIPMYFFLAILSC  
 SEICYTFIIVPKMLVDLLSQKKTISFLGCAIQMFSFLFLGCSHSFLLAVMGYDRYIAICNPLRYSV  
 LMGHGVCMGLVAAACACGFTVAQIITSLVFHLPFYSSNQLHFFCDIAPVLKLASHHNHFSQIV  
 IFMLCTLVLAIPLLLILVSYVHLSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASFIYLRPQSNY  
 SSSQDALISVSYTIITPLFNPMIYSLRNKEFKSALCKIVRRRTISLL (SEQ ID NO: 185)

25   ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTCATCTTCCTCGGCTTCTCATCCCTGG  
 CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCCTGCTCCTCTACCTGTTCACTCTGGGCACC  
 AATGCAATCATCATTTCCACCATTGTCTGGACAGGGCCCTTCATATCCCCATGTACTTCTT  
 CCTTGCCATCCTCTCTTGCTCTGAGATTTGCTACACCTTCATCATTGTACCCAAGATGCTGG  
 TTGACCTGCTGTCCCAGAAGAAGACCATTTCTTTCTGGGCTGTGCCATCCAAATGTTTTCC  
 TTCCTCTTCCTTGGCTGCTCTCACTCCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT  
 30   AGCCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTGTATGGGACTA  
 GTGGCTGCTGCCTGTGCCTGTGGCTTCACTGTTGCACAGATCATCACATCCTTGGTATTTC  
 CCTGCCTTTTTATTCCCTCCAATCAACTACATCACTTCTTCTGTGACATTGCTCCTGTCCCTCA  
 AGCTGGCATCTCACCATAACCACTTTAGTCAGATTGTATCTTCATGCTCTGTACATTGGTC  
 CTGGCTATCCCCCTATTGTTGATCTTGGTGTCTATGTTACATCCTCTCTGCCATACTTCA  
 GTTTCCTTCCACACTGGGTAGGTGCAAAGCTTTTCTACCTGTGTATCTCACCTATTATG  
 35   TCACTGTCCACTATGGCTGTGCCTCCTTTATCTACTTAAAGGCCTCAGTCCAACTACTCCTCA  
 AGCCAGGATGCTCTAATATCAGTATCCTTACACTATTATAACTCCATTGTTCAACCCAATGA  
 TTTATAGCTTGAGAAATAAGAGTTCAAATCAGCTCTTTGTAAAATTGTGAGAAGAACAAAT  
 TTCCTGTGTGTA (SEQ ID NO: 186)

**AOLFR101 sequences:**

40   MDTGNWSQVAEFILGFPHLQGVQIYLFLLLLLIYLMTVLGNLLIFLVVCLDSRLHTPMYHFVSI  
 LSFSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL  
 HYPTLMTPTLCAEIAIGCWLGGLAGPVVEISLISRLPFCGPNRIQHVFCDPFPVLSLACTDTSINV  
 LVDFVINSCKILATFLLILCSYVQIICTVLRIPSAAGKRKAISTCASHFTVVLIFYGSILSMYVQLK  
 45   KSYSLDYDQALAVVYSVLTPFLNPFYISLRNKEIKEAVRRQLKRIGILA (SEQ ID NO: 187)

50   ATGGACACAGGGA ACTGGAGCCAGGTAGCAGAATTCATCATCTTGGGCTTCCCCCATCTCC  
 AGGGTGTCCAGATTTATCTCTTCTCTTGTGCTTCTCATTTACCTCATGACTGTGTTGGGA  
 AACCTGCTGATATTCCTGGTGGTCTGCCTGGACTCCCGGCTTCACACACCCATGTACCACT  
 TTGTCAGCAATCTCTCCTTCTCAGAGCTTGGCTATACAGCTGCCACCATCCCTAAGATGCTG  
 GCAAACATTGCTCAGTGAGAAAAAGACCATTTTATTCTCTGGGTGTCTCCTGCAGATCTATT  
 TCTTTCACTCCCTTGGAGCGACTGAGTGCTATCTCCTGACAGCTATGGCCTACGATAGGTA  
 TTTAGCCATCTGCCGGCCCCCTCCACTACCCAACCCTCATGACCCCAACACTTTGTGCAGAG  
 ATTGCCATTGGCTGTTGGTTGGGAGGCTTGGCTGGGCCAGTAGTTGAAATTTCTTGATTT  
 55   CACGCCTCCCATCTGTGGCCCCAATCGCATTACAGCACGTCTTTGTGACTTCCCTCCTGTG  
 CTGAGTTTGGCTTGCACTGATACGTCTATAAATGTCCTAGTAGATTTTGTATAAATTCCTG



**AOLFR105 sequences:**

MQGLNHTSVSEFILVGFSAPHLQLMLFLLFLLMYLFTLLGNLLIMATVWSESLHMPMYLFLC  
ALSITEILYTVAIIPRMLADLLSTQRSIAFLACASQMFFSFSFGFTHSFLLTVMGYDRYVAICHPL  
RYNVLM SLRGCTCRVGCSWAGGLVMGMVVTSAIFHLAFCGHKEIHHFFCHVPPLLKLACGDD  
5 VLVVAKGVGLVCITALLGCFLILLISYAFIVAAILKIPSAEGRNKAFTSCASHLTVVVVHYGFAS  
VIYLKPKGPQSPGDTLMGITYTVLTPFLSPIIFSLRNKELKVAMKKTCTFKLFPQNC (SEQ ID  
NO: 193)

10 ATGCAGGGGCTAAACCACACCTCCGTGTCTGAATTCATCCTCGTTGGCTTCTCTGCCTTCCC  
CCACCTCCAGCTGATGCTCTTCCTGCTGTTCTGCTGATGTACCTGTTACGCTGCTGGGCA  
ACCTGCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCCATGTACCTCTT  
CCTGTGTGCCCTCTCCATCACCGAGATCCTCTACACCGTGGCCATCATCCCGCGCATGCTG  
GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTTCTGTCCTGTGCCAGTCAGATGTTCTT  
CTCCTTCAGCTTCGGCTTCACCCACTCCTTCTGCTCACTGTCATGGGCTACGACCGCTACG  
15 TGGCCATCTGCCACCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG  
GGTGGGCTGCTCCTGGGCTGGTGGCTGATGGGGATGGTGGTGACCTCGGCCATTTTC  
CACCTCGCCTTCTGTGGACACAAGGAGATCCACCATTCTTCTGCCACGTGCCACCTCTGTT  
GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGTAT  
CACGGCCCTGCTGGGCTGTTTTCTCTCATCCTCCTCTCCTATGCCTTCATCGTGGCCGCCA  
20 TCTTGAAGATCCCTTCTGCTGAAGGTCGGAACAAGGCCTTCTCCACCTGTGCCTCTCACCT  
CACTGTGGTGGTGCCTGACTATGGCTTTCCTCCGTCATTTACCTGAAGCCCAAAGGTCCC  
CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACCTACACGGTCTCACACCCTTCTCA  
GCCCCATCATCTTCAGCCTCAGGAACAAGGAGCTGAAGGTCGCCATGAAGAAGACTTGCTT  
CACCAAACCTTTCCACAGAACTGCTGA (SEQ ID NO: 194)

25

**AOLFR106 sequences:**

METANYTKVTEFVLTGLSQTPEVQLVLFVIFLSFYLFILPGNIICTISLDPHLTSPMYFLLANLA  
FLDIWYSSITAPEMLIDFFVERKISFDGCIQLFFLHFAGASEMFLLTVMFAFDLYTAICRPLHYA  
TIMNQRLCCILVALSWRGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM  
30 ICSSGLISVVCLIALLSYAFLLALFKKLSGSGENTNRAMSTCYSHITIVVLMFGPSIYIYARPD  
SFSLDKVVSVFNTLIFPLRNPIIYTLRNKEVKAAMRKLVTKYILCKEK (SEQ ID NO: 195)

35 ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC  
CAGAGGTCCAACTAGTCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA  
AATATCCTTATCATTTGCACCATCAGTCTAGACCCTCATCTGACCTCTCCTATGTATTCTCT  
GTTGGCTAATCTGGCCTTCTTGATATTTGGTACTCTTCCATTACAGCCCCTGAAATGCTCA  
TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTTGATGGATGCATTGCACAGCTCTTCTT  
CTTACACTTTGCTGGGGCTTCGGAGATGTTCTTGCTCACAGTGATGGCCTTTGACCTCTACA  
CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGTCTCTGCTGTATCCTG  
40 GTGGCTCTCTCCTGGAGGGGGGGGCTTCATTCATTCTATCATACAGGTGGCTCTCATTGTT  
GACTTCCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTGT  
CCGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCTG  
ATCTCTGTGGTGTGTTTGATTGCTCTGTTAATGTCCTATGCCTTCTTCTGGCCTTGTTC  
GAAACTTTACAGGCTCAGGTGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACATT  
45 ACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTGACTCGTT  
TTCCCTAGATAAAGTGGTGTCTGTGTTCAATACTTTAATATTCCTTTACGTAATCCCATT  
TTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTTGGTCACCAAATATA  
TTTTGTGTAAAGAGAAGTGA (SEQ ID NO: 196)

**AOLFR107 sequences:**

MELWNFTLGSFILVIGILNDSGSPELLCATITILYLLALISNGLLLLAITMEARLHMPMYLLLGQ  
LSLMDLLFTSVVTPKALADFLRRENTISFGGALQMFLALTMGGAEDLLAFMAYDRYVAICH  
PLTYMTLMSSRACWLMVATSWILASLSALIYTVYTMHYPFCRAQEIRHLLCEIPHLLKVACAD  
TSRYELMVYVMGVTFILPSLAAILASYTQILLTVLHMPSPNEGRKKALVTCSSHLTVMGMFYGA  
55 ATFMVYLPSSFHSTRQDNIIISVFYITVTPALNPLIYSLRNKEVMRALRRVLGKYMLPAHSTL  
(SEQ ID NO: 197)

ATGGAGCTCTGGAACCTTCACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA  
 GTGGGTCTCCTGAACTGCTCTGTGCTACAATTACAATCCTATACTTGTGGCCCTGATCAG  
 CAATGGCCTACTGCTCCTGGCTATCACCATGGAAGCCCGGCTCCACATGCCCATGTACCTC  
 5 CTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTACATCTGTTGTCACTCCCAAGGCCCT  
 TGGCGACTTTCTGCGCAGAGAAAACACCATCTCCTTTGGAGGCTGTGCCCTTCAGATGTTT  
 CTGGCACTGACAATGGGTGGTGGTCTGAGGACCTCCTACTGGCCTTCATGGCCTATGACAGGT  
 ATGTGGCCATTTGTCTATCCTCTGACATACATGACCCTCATGAGCTCAAGAGCCTGCTGGCT  
 CATGGTGGCCACGTCTTGGATCCTGGCATCCCTAAGTGCCCTAATATATACCGTGTATACC  
 10 ATGCACTATCCCTTCTGCAGGGCCCAGGAGATCAGGCATCTTCTCTGTGAGATCCACACT  
 TGCTGAAGGTGGCCTGTGCTGATACCTCCAGATATGAGCTCATGGTATATGTGATGGGTGT  
 GACCTTCCTGATTCCCTCTCTTGTCTGCTATACTGGCCTCCTATACACAAATTCTACTACTG  
 TGCTCCATATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTCACTGCTCTTCCACCT  
 GACTGTGGTTGGGATGTTCTATGGAGCTGCCACATTCATGTATGTCTTGCCAGTTCTCTCC  
 15 ACAGCACCAGACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAA  
 TCCACTCATCTACAGCCTGAGGAATAAGGAGGTTCATGCGGCCCTTGAGGAGGGTCTGGG  
 AAAATACATGCTGCCAGCACACTCCACGCTCTAG (SEQ ID NO: 198)

**AOLFR108 sequences:**

20 MCSFFLCQTKQKAKISMGEENQTFVSKFIFLGLSQDLQTQILLFILFLIHYLLTVLGNQLIILIFLD  
 SRLHTPMYFFLRNLSFADLCFSTSIVPQVLVHFLVKRKTISFYGCMTQIIVFLLVGCTECALLAV  
 MSYDRYVAVCKPLYYSTIMTQVRVCLWLSFRSWASGALVSLVDSFTFHLPLYWGQNIINHYFCE  
 PPALLKLASIDTYSTEMAIFSMGVVILLAPVSLILGSYWNIISTVIQMQSGEGRLLKAFSTCGSHLI  
 25 VVVLFGSGIFTYMRPNSKTTKELDKMISVFYTAVTPMLNPIIYSLRNKDVKGALRKLVGRC  
 FSHRQ (SEQ ID NO: 199)

ATGTGTTCTTTTTTCTTGTGCCAAACAGGTAAACAGGCAAAAATATCAATGGGAGAAGAAA  
 ACCAAACCTTTGTGTCCAAGTTTATCTTCCTGGGTCTTTCACAGGACTTGCAGACCCAGAT  
 CCTGCTATTTATCCTTTTCTCATCATTTATCTGCTGACCGTGCTTGGAACCCAGCTCATCA  
 30 TCATTCTCATCTTCTGATTCTCGCCTTCACACTCCCATGTATTTTTTCTTAGAAATCTCT  
 CCTTTCAGATCTCTGTTTCTCTACTAGCATTGTCCCTCAAGTGTGGTTCACTTCTTGTA  
 AAGAGGAAAACCATTTCTTTTTATGGGTGTATGACACAGATAATTGTCTTTCTTCTGGTTG  
 GGTGTACAGAGTGTGCGCTGCTGGCAGTGATGTCCTATGACCGGTATGTGGCTGTCTGCAA  
 GCCCCTGTACTACTTACCATCATGACACAACGGGTGTGTCTCTGGCTGTCTTCCAGTCCCT  
 35 GGGCCAGTGGGGCACTAGTGTCTTTAGTAGATACCAGCTTTACTTTCCATCTTCCCTACTG  
 GGGACAGAATATAATCAATCACTACTTTTGTGAACCTCCTGCCCTCCTGAAGCTGGCTTCC  
 ATAGACACTTACAGCACAGAAATGGCCATCTTTTCAATGGGCGTGGAATCCTCCTGGCCC  
 CTGTCTCCCTGATTCTTGGTTCTTATTGGAATATTATCTCCACTGTTATCCAGATGCAGTCT  
 GGGGAAGGGAGACTCAAGGCTTTTCCACCTGTGGCTCCCATCTTATTGTTGTTGTCCTCTT  
 40 CTATGGGTCAGGAATATTCACCTACATGCGACCAAACCTCCAAGACTACAAAAGAACTGGA  
 TAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCCATATTTATAGC  
 TTGAGGAACAAAGATGTCAAAGGGGCTCTCAGGAAACTAGTTGGGAGAAAGTGCTTCTCT  
 CATAGGCAGTGA (SEQ ID NO: 200)

**AOLFR109 sequences:**

45 MLRNGSIVTEFILVGFQSSSTSTRALLFALFLALYSLTAMNGLIIFITSWTDPKLNSPMYFFLG  
 HLLLDVCFITTTIPQMLIHLVVRDHIVSFVCCMTQMYFVFCVGVAECILLAFMAYDRYVAICY  
 PLNYVPIISQKVCVRLVGTAWFFGLINGIFLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPQFSL  
 WAIFADAIVVLSPMVLTVTSYVHILATILSKASSSGRGKTFSTCASHLTVVIFLYTSAMFSYMN  
 50 PHSTHGPKDKPFSLLYTIITPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPQSV (SEQ ID NO:  
 201)

ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTCAGCAGAGCTCCA  
 CTTCCACACGAGCATTGCTCTTTGCCCTCTTCTGGCCCTCTACAGCCTCACCATGGCCATG  
 55 AATGGCCTCATCATCTTTATCACTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTA  
 TCTTCTCGGCCATCTGTCTCTCCTGGATGTCTGCTTCATCACCCTACCATCCACAGATG

TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT  
 ACTTTGTCTTCTGTGTTGGTGTGGCCGAGTGCATCCTCTTGGCTTTTCATGGCCTATGACCGT  
 TATGTTGCTATCTGCTACCCACTTAACATATGTCCCGATCATAAGCCAGAAGGTCTGTGTCA  
 GGCTTGTGGGAAGTGCCTGGTTCTTTGGGCTGATCAATGGCATCTTCTCGAGTATATTTT  
 5 ATCCGAGAGCCCTTCCGAGAGACAACCACATAGAAAGCTTCTTCTGTGAGGCCCCCATA  
 GTGATTGGCCTCTCTTGTGGGGACCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA  
 TCGTGGTAATTCTCAGCCCCATGGTGCTCACTGTCACTTCCTATGTGCACATCCTGGCCACC  
 ATCCTCAGCAAAGCCTCCTCCTCAGGTCGGGGGAAGACTTTCTACTTGTGCCTCTCACC  
 TGA CTGTGGTCACTTTCTCTACACTTCAGCTATGTTCTCTTACATGAACCCCCACAGCACA  
 10 CATGGGCTGACAAAGACAAACCTTTCTCCCTCCTGTACACCATCATTACCCCCATGTGCA  
 ACCCATCATTTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTG  
 GAAGAACCAGGCTGGCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

**AOLFR110 sequences:**

15 MKIANNTVVTEFILLGLTQSQDIQLLVFVLILIFYLILPGNFLIIFTIRSDPGLTAPLYLFLGNLAFL  
 DASYSFIVAPRMLVDFLSEKKVISYRGCTQLFFLHFLGGEGLLLVMAFDRIAICRPLHCST  
 VMNPRACYAMMLALWLGGFVHSIIQVVLRLPFCGPNQLDNFFCDVRQVIKLACTDMFVVEL  
 LMVFNGLMTLLCFLGLLASYA VILCHVRRRAASEGKNKAMSTCTTRVIIIIMFGPAIFIYMCPP  
 20 RALPADKMVSLFHTVIFPLMNPMIYTLRNQEVKTSMKRLLSRHVVCQVDFIIRN (SEQ ID NO:  
 203)

ATGAAGATAGCAAACAACACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC  
 AAGATATTCAGCTCTTGGTCTTGTGCTGATCTTAATTTCTACCTTATCATCCTCCCTGGA  
 AATTTTCTCATTATTTTACCATAAGGTCAGACCCTGGGCTCACAGCCCCCTCTATTTATT  
 25 TCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTCATTGTGGCTCCCAGGATGTTGG  
 TGGACTTCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTTT  
 CTTGCACTTCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTAC  
 ATCGCCATCTGCCGGCCTCTGCACTGTTCAACTGTGATGAACCCTAGAGCCTGCTATGCAA  
 TGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCCCTCATCCTC  
 30 CGCTTGCCCTTTTTGTGGCCCAAACCAGCTGGACAACCTTCTTCTGTGATGTCCGACAGGTCA  
 TCAAGCTGGCTTGCACCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT  
 GATGACACTCCTGTGCTTTCTGGGGCTTCTGGCTTCTATGCAGTCATCCTCTGCCATGTTCT  
 GTAGGGCAGCTTCTGAAGGGAAGAACAAGGCCATGTCCACGTGCACCACTCGTGTGATTA  
 TTATACTTCTTATGTTTGGACCTGCTATCTTACATGATGTGCCCTTTCAGGGCCTTACCA  
 35 GCTGACAAGATGGTTTCTCTCTTTCACACAGTGATCTTCCATTGATGAATCCTATGATTTA  
 TACCCTTCGCAACCAGGAAGTGAAAACCTCCATGAAGAGGTTATTGAGTCGACATGTAGTC  
 TGTCAAGTGGATTTTATAATAAGAACTGA (SEQ ID NO: 204)

**AOLFR111 sequences:**

40 MCYIYLIFKEWTLIFYFSLLLFLQITPAIMANLTIVTEFILMGFSTNKNMCILHSILFLIYL CALM  
 GNVLIIMITLDDHLHTPVYFFLKNLSFLDLCLISVTAPKSIANSIHNNSISFLGCVSQVFLLLSS  
 ASAEILLLTVMSEFDRTAICHPLHYDVIMDRSTCVQRATVSWLYGGIAVMHTAGTFSLSYCG  
 SNMVHQFFCDIPQLLAISCSENLI REIALILINVLDFCCFIVIIITYVHVSTVKKIPSTEGQSKAY  
 45 SICLPHLLVVLSTGFIAYLKPASESPSILDAVISVFYTM LPPTFNPIIYSLRNKAIKVALGMLIKG  
 KLTKK (SEQ ID NO: 205)

ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT  
 TTTCTGAGATTACTCCTGCAATAATGGCAAATCTCACAATCGTGACTGAATTTATCCTTA  
 TGGGGTTTTCTACCAATAAAAAATATGTGATTTTGCATTTCGATTCTCTTCTTGTGATTTAT  
 50 TTGTGTGCCCTGATGGGGAATGTCCTCATTATCATGATCACAACCTTTGGACCATCATCTCC  
 ACACCCCCGTGTATTTCTTCTTGAAGAATCTATCTTTCTTGGATCTCTGCCTTATTTAGTC  
 ACGGCTCCCAAATCTATCGCCAATTCTTTGATACACAACAACCTCCATTTCATTCTTGGCTG  
 TGTTTCCCAGGTCCTTTTGTGCTTTCTTACGATCTGCAGAGCTGCTCCTCCTACGGTGA  
 TGTCCTTTGACCGCTATACTGCTATATGTCACCCTCTGCACTATGATGTGATCATGGACAGG  
 55 AGCACCTGTGTCCAAAGAGCCACTGTGTCTTGGCTGTATGGGGGTCTGATTGCTGTGATGC  
 ACACAGCTGGCACCTTCTCCTTATCCTACTGTGGGTCCAACATGGTCCATCAGTTCTTCTGT

GACATTCCCCAGTTATTAGCTATTTCTTGCTCAGAAAATTTAATAAGAGAAATTGCACTCA  
 TCCTTATTAATGTAGTTTTGGATTTCTGCTGTTTTATTGTCATCATCATTACCTATGTCCAC  
 GTCTTCTCTACAGTCAAGAAGATCCCTTCCACAGAAGGCCAGTCAAAAGCCTACTCTATTT  
 GCCTTCCACACTTGCTGGTTGTGTTATTTCTTTCCACTGGATTCAATTGCTTATCTGAAGCCA  
 5 GCTTCAGAGTCTCCTTCTATTTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCCC  
 AACCTTTAATCCCATATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG  
 TTGATAAAGGGAAAGCTCACAAAAAGTAA (SEQ ID NO: 206)

**AOLFR113 sequences:**

10 MKFWHGFSSHLNPMFSSFLLYLSLPWINTTIQAWLNLCALPVWAMSGAGFLSCCYWHTCSP  
 SVVTCSSSQSSDWMQLCTHLCTTSLVFFPSWSCGIQLPLSLRCLIFSRRKPFLLQDASFRPTSS  
 TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTTLCAKMAAACWTCGFLCPISEVILASQLPF  
 CAYNEIQHIFCDPPLSLACKDTSANILVDFAINAFILITFFMISYARIIGAVLKIKTASGRKK  
 AFSTCASHLAVVLIFFGSIIFMYVRLKKSYSLTLDRTLAIVYSVLTMPVMNPIIYSLRNKEIHKAIKR  
 15 TIFQKGDKASLAHL (SEQ ID NO: 207)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA  
 AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC  
 CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA  
 20 GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA  
 TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA  
 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG  
 CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG  
 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA  
 25 GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT  
 AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT  
 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA  
 GCAGTCTCTACAGTCTGATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT  
 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA  
 30 AGCATTAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG  
 GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACCCCAAGTCTGC  
 TAGCTGACCTGTACGTGATCATCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC  
 CAAACAACCTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCTCTTTGACCATTCCAAC  
 CTGGGTTTCATGA (SEQ ID NO: 208)

35

**AOLFR114 sequences:**

MERINHSSVSEFILLGLSSRPEDQKTLFVLFLIVYLVTTITGNLLIHLAIRFNPHLQTPMYFFLSFLS  
 LTDICFTTSVVPKMLMNLSEKKTISYAGCLTQMYFLYALGNSDSLAVMAFDYVAVCDPF  
 HYVTTMSHHHCVLLVAFSCSFPHLHSLHTLLNRLTFCDNSVIHHFLCDLSPVLKLSCSSIFVN  
 40 EIVQMTEAPIVLVTRFLCIAFSYIRILTVLKIPSTSGKRKAFSTCGFYLTVVTLFYGSIFCVYLQP  
 PSTYAVKDHVATIVYTVLSSMLNPFIYSLRNKDLKQGLRKLMSKRS (SEQ ID NO: 209)

ATGGAAAGAATCAACCACACCAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCCTCCC  
 GGCCTGAGGACCAAAAGACACTCTTTGTTCTCTTCCTCATCGTGACCTGGTCACCATAAC  
 45 AGGGAACCTGCTCATCATCCTGGCCATTGCTTCAACCCCCATCTTCAGACCCCTATGTATT  
 TCTTCTTGAGTTTTCTGTCTCTCACTGATATTTGCTTTACAACAAGCGTTGTCCCCAAGATG  
 CTGATGAACCTCCTGTGAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACACAGATGT  
 ATTTTCTCTATGCCTTGGGCAACAGTGACAGCTGCCTTCTGGCAGTCATGGCCTTTGACCG  
 CTATGTGGCCGTCTGTGACCCCTTCCACTATGTACCACCATGAGCCACCACCATGTGTCTC  
 50 TGCTGGTGGCCTTCTCCTGCTCATTTCTCCTCACTCCTGACACACTTCTGCTG  
 AATCGTCTACCTTCTGTGACTCCAATGTTATCCACCACCTTCTCTGTGACCTCAGCCCTGT  
 GCTGAAATTGTCCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACAGAAGCACCT  
 ATTGTTTTGGTGACTCGTTTTCTCTGCATTGCTTTCTCTTATATACGAATCCTCACTACAGT  
 TCTCAAGATTCCCTCTACTTCTGGGAAACGAAAGCCTTCTCCACCTGTGGTTTTTACCTCA  
 55 CCGTGGTGACGCTCTTTTATGGAAGCATCTTCTGTGTCTATTACAGCCCCCATCCACCTAC  
 GCTGTCAAGGACCACGTGGCAACAATTGTTTACACAGTTTTGTCTCATCATGCTCAATCCTT

TTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCAAGA  
GATCCTAG (SEQ ID NO: 210)

**AOLFR115 sequences:**

5 MEGFYLRSHLQGMGKPGRVNQTTVSDFLLLGLSEWPPEEQPLLFGIFLGMVLTVMVGNLLII  
LAISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLLMFGGLD  
NCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVLTNCPALMHTLLLTRVAFCAQK  
AIPHFYCDPSALLKLACSDTHVNELMIITMGLLFLTVPLLLIVFSYVRIFWAVFVISSPGGRWKA  
FSTCGSHLTVVLLFYGSLMGVYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLNRNMDKEALG  
10 KLFVSGKTFFL (SEQ ID NO: 211)

ATGGAAGGTTTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACCAGGCAGA  
GTGAACCAAACCACTGTTTCAGACTTCCTCCTTCTAGGACTCTCTGAGTGGCCAGAGGAGC  
AGCCTCTTCTGTTTGGCATCTTCCTTGGCATGTACCTGGTCACCATGGTGGGGAACCTGCTC  
15 ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATACTCCCATGTACTTCTTTCTGGCCAA  
CCTGTCATTAACTGATGCCTGTTTCACTTCTGCCTCCATCCCCAAAATGCTGGCCAACATTC  
ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGTCTTGACACAGCTATATTTCTCCTTATG  
TTTGGTGGCCTTGACAACTGCCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT  
GCCAACCACTCCATTACAGCACATCTATGAGTCCCCAGCTCTGTGCACTAATGCTGGGTGT  
20 GTGCTGGGTGCTAACCACTGTCCTGCCCTGATGCACACACTGTTGCTGACCCGCGTGGCT  
TTCTGTGCCAGAAAGCCATCCCTCATTCTATTGTGATCCTAGTGCTCTCCTGAAGCTTGC  
CTGCTCAGATACCCATGTAACGAGCTGATGATCATCACCATGGGCTTGCTGTTCTCTCACT  
GTTCCTCCTGCTGATCGTCTTCTCTATGTCCGCATTTTCTGGGCTGTGTTTGTCTATCTC  
ATCTCCTGGAGGGAGATGGAAGGCCTTCTCTACCTGTGGTTCTCATCTCAGCGTGGTTCTG  
25 CTCTTCTATGGGTCTCTTATGGGTGTGATTTACTTCTCCATCAACTTACTCTACAGAGAG  
GGAAAGTAGGGCTGCTGTTCTCTATATGGTGATTATCCCACGCTAAACCCATTCAATTTAT  
AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAAACTTTTTGTCAGTGGAAAAACA  
TTCTTTTTATGA (SEQ ID NO: 212)

**AOLFR116 sequences:**

30 MDEANHSVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFLLAN  
LSIINLVFCSSTAPKMIYDLFRKHKTISFGGCVVQIFFIHAVGGTEMVLLIAMAFDRYVAICKPLH  
YLTIMNPQRCLFLVISWIIHHSVIQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV  
TANSGFISLASFLILISYIFILVTVQKKSSGGIFKAFSMLSAHVIVVVLVFGPLIFFYIFPPTSHLD  
35 KFLAIFDAVITPVLNPVIYTFRNKEMMVAMRRRCSQFVNYSKIF (SEQ ID NO: 213)

ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTCTGTTGACTCTCTGACTCGC  
GGAAGATCCAGCTCCTCCTCTTCTCTTTTCTCAGTGTTCTATGTATCAAGCCTGATGGGA  
AATCTCCTCATTGTGCTAACTGTGACCTCTGACCCTCGTTTACAGTCCCCCATGTACTTCCT  
40 GCTGGCCAACCTTTCCATCATCAATTTGGTATTTTGTCTCCACAGCTCCCAAGATGATTT  
ATGACCTTTTCAGGAAGCACAAAGACCATCTCTTTTGGGGGCTGTGTAGTTTCAATCTTCTT  
TATCCATGCAGTTGGGGGAACTGAGATGGTGCTGCTCATAGCCATGGCTTTTGACCGATAT  
GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTTTGT  
TTTTAGTCATTTCTGATTATAGGTATTATCACTCAGTGATTGAGTTGGCTTTTGTGTTGTA  
45 GACCTGCTGTTCTGTGGCCCTAATGAATTAGATAGTTTCTTTTGTGATCTTCTCGATTTAT  
CAAACCTGGCTTGCTAGAGACCTACACATTGGGATTTCATGGTTACTGCCAATAGTGGATTT  
ATTCTCTGGCTTCTTTTAAATTCTCATAATCTCTTACATCTTTATTTTGGTGACTGTTTCAG  
AAAAAATCTTCAGGTGGTATATTCAAGGCTTTCTCTATGCTGTCAGCTCATGTCATTGTG  
TGGTTTTGGTCTTTGGGCCATTAATCTTTTCTATATTTTCCATTTCCACATCACATCTTG  
50 ATAAATTCCTTGCCATCTTTGATGCAGTTATCACTCCCGTTTGAATCCAGTCATCTATACT  
TTTAGAAATAAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTAC  
AGTAAATCTTTTAA (SEQ ID NO: 214)

**AOLFR117 sequences:**

55 MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLLVISRLLLAMTLGNSTEVTEFYLLGFGA  
QHEFWCILFIVFLLIYVTSIMGNSGIILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSFT

EEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPYVAICKPLHYTVIMSRTVCIRLVAGSYI  
MGSINASVQTGFTCSLSFCKSNSINHHFCDVPPILALSCSNVDINIMLLVVFVGSNLIFTGLVVIFS  
YIYIMATILKMSSSAGRKKSFSSTCASHLTAVTIFYGTLSYMYLQSHSNNSQENMKVAFIFYGTVI  
PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215)

5

ATGAATAACACTATTGTATTTGTCATAAAAAATACAAATAGAAAAAAGTGACTTGAAATATA  
GAGCCATTTTCATTGCAAGAAATCTCAAAGATTTCCCTTCTTTTCTGGGTCCTTCTCTTGGTC  
ATTTCTAGACTTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTCTATC  
TTCTGGGATTTGGTGCCAGCATGAGTTTTGGTGTATCCTCTTCATTGTATTCCTTCTCATC  
10 TATGTGACCTCCATAATGGGTAATAGTGGAATAATCTTACTCATCAACACAGATTCCAGAT  
TTCAAACACTCACGTACTTTTTTCTACAACATTTGGCTTTTGGTTGATATCTGTTACACTTCT  
GCTATCACTCCCAAGATGCTCCAAAGCTTCACAGAAGAAAAGAATTTGATATTATTTTCAGG  
GCTGTGTGATACAATTCTTAGTTTATGCAACATTTGCAACCAGTGACTGTTATCTCCTGGCT  
ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCCTTCACTATACTGTAATCATGT  
15 CCCGAACAGTCTGCATCCGTTTGGTAGCTGGTTCATACATCATGGGCTCAATAAATGCCTC  
TGTACAAAACAGGTTTTACATGTTCACTGTCCTTCTGCAAGTCCAATAGCATCAATCACTTTT  
TCTGTGATGTTCCCCCTATTCTTGCTCTTTTCATGCTCCAATGTTGACATCAACATCATGCTA  
CTTGTTGTCTTTGTGGGATCTAACTTGATTTCACTGGGTTGGTCGTCATCTTTTCTACAT  
CTACATCATGGCCACCATCCTGAAAATGTCTTCTAGTGCAGGAAGGAAAAAATCCTTCTCA  
20 ACATGTGCTTCCACCTGACCGCAGTCACCATTTTCTATGGGACACTCTCTTACATGTATTT  
GCAGTCTCATCTAATAATTCCAGGAAAATATGAAAGTGGCCTTTATATTTTATGGCACA  
GTTATTCCCATGTTAAATCCTTTAATCTATAGCTTGAGAAATAAGGAAGTAAAAGAAGCTT  
TAAAGTGATAGGGAAAAAGTTATTTTAA (SEQ ID NO: 216)

25 **AOLFR118 sequences:**

MNHMSASLKISNSSKFQVSEFILLGFPGIHSWQHWLSLPLALLYLSALAANTLILIIWQNPSLQQ  
PMYIFLGILCMVDMGLATTIIPKILAFWFDAKVISLPECFAQIYAIHFFVGMESGILLCMAFDY  
VAICHPLRYPISIVTSSILKATLFMVLNRNGLFVTPVPVLAQRDYCSKNEIEHCLCSNLGVTSLA  
CDDRRPNISICQLVLAWLGMGSDLSLILSYLILYSVLRNSAEAAAKALSTCSSHLTLILFFYTIV  
30 VVISVTHLTEMKATLIPVLLNVLHNIIPPSLNPTVYALQTKELRAAFQKVLFAITKEIRS (SEQ ID  
NO: 217)

ATGAATCATATGTCTGCATCTCTCAAAATCTCCAATAGCTCCAAATTCAGGTCTCTGAGTT  
CATCCTGCTGGGATTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCTGGCA  
35 CTACTGTATCTCTCAGCACTTGCTGCAAACACCCTCATCCTCATCATCTGGCAGAACCC  
TTCTTTACAGCAGCCCATGTATATTTTCTTGGCATCCTCTGTATGGTAGACATGGGTCTGG  
CCACTACTATCATCCCTAAGATCCTGGCCATCTTCTGGTTTGATGCCAAGGTTATTAGCCTC  
CCTGAGTGCTTTGCTCAGATTTATGCCATTCACTTCTTTGTGGGCATGGAGTCTGGTATCCT  
ACTGTCATGGCTTTTGATAGATATGTGGCTATTTGTCACCCTCTTCGCTATCCATCAATTG  
40 TCACCAGTTCCTTAATCTTAAAAGCTACCCTGTTTCATGGTGCTGAGAAATGGCTTATTTGTC  
ACTCCAGTGCCTGTGCTTGACAGCACAGCGTGATTATTGCTCCAAGAATGAAATTGAACACT  
GCCTGTGCTCTAACCTTGGGGTCACAAGCCTGGCTTGTGATGACAGGAGGCCAAACAGCAT  
TTGCCAGTTGGTTCTGGCATGGCTTGAATGGGGAGTGATCTAAGTCTTATTATACTGTCA  
TATATTTTGATTCTGTACTCTGTACTTAGACTGAACTCAGCTGAAGCTGCAGCCAAGGCC  
45 TGAGCACTTGTAGTTCACATCTCACCTCATCCTTTTCTTTTACACTATTGTTGTAGTGATT  
TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATTCCAGTTCTACTTAATGTGTTGC  
ACAACATCATCCCCCTTCCCTCAACCCTACAGTTTATGCACTTCAGACCAAAGAACTTAG  
GGCAGCCTTCCAAAAGGTGCTGTTTGCCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:  
218)

50

**AOLFR119 sequences:**

MPLFNSLCWFPTIHVTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP  
MYFFFGHALSLIDLLTCTTTLPNALCIFWFSKEINFNACLAQMFFVHGFTGVESGVLMLMALD  
RYIAICYPLRYATTLNPIIAKAEATFLRGVLLMIPFPFLVKRLPFCQSNIIISHTYCDHMSVVKL  
55 SCASIKVNVYGLMVALLIGVFDICISLSYTLILKAAISLSSSDARQKAFSTCTAHISAIITYVPA



FFTTFAHRFGGHTIPPSLHIIIVANLYLLPPTLNPIVYGVKTKQIRKSVIKFFQGDKGAG (SEQ ID NO: 219)

5 ATGCCTCTATTTAATTCATTATGCTGGTTTCCAACAATTCATGTGACTCCTCCATCTTTTAT  
TCTTAATGGAATACCTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCCACTCTGCACA  
ATGTACATCATCTTCCTTGTGGGAATCTTGGTCTTGTGTACCTCATTTATTATGAGGAGTC  
CTTACATCATCCGATGTATTTTTTTTTTGGCCATGCTCTCTCCCTCATTGACCTCCTTACCTG  
CACCACCACTCTACCCAATGCACTCTGCATCTTCTGGTTCAGTCTCAAAGAAATTAACCTCA  
ATGCTTGCTTGGCCCAGATGTTCTTTGTTCATGGGTTACAGGTGTGGAGTCTGGGGTGCT  
10 CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCCTTTGCGTTATGCTACCACAC  
TCACCAACCCTATCATTGCCAAGGCTGAGCTTGCCACCTTCCTGAGGGGTGTATTGCTGAT  
GATTCCTTTCCCATCTTGGTTAAGCGTTTGCCTTTCTGCCAAAGCAATATTATCTCCATA  
CGTACTGCGACCACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT  
CTATGGTCTAATGGTTGCTCTCCTGATTGGAGTGTGTGACATTTGTTGTATATCTTTGTCTT  
15 ACACCTTGATCCTCAAGGCAGCGATCAGCCTCTCTTCATCAGATGCTCGGCAGAAGGCTTT  
CAGCACTGCACTGCCATATATCTGCCATCATCATCACCTATGTTCCAGCATTCTTCACTT  
TCTTTGCCACCGTTTGGGGGACACACAATTCCCCCTTCTCTTCACATCATTGTGGCTAAT  
CTTTATCTTCTTCTTCCCCCACTCTAAACCCTATTGTTTATGGAGTAAAGACAAAACAGAT  
ACGCAAGAGTGTCTATAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGA (SEQ ID NO: 220)

20

**AOLFR120 sequences:**

MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENLAAILVGLDHLRRLRPMYF  
FLTHLSCLEIWYTSVTPVKMLAGFIGVDGGKNISYAGCLSQLFIFTLGATECFLLAAMAYDRY  
VAICMPLHYGAFVSWGTCIRLAAACWLVGFLTPIPLIYLLSQLTFCGPNVIDHFSCDASPLLALS  
25 CSDVTWKETVDFLVSLAVLLASSMVIASVYGNIVWTLHIRSAAERWKAFSTCAHLTVVSLF  
YGTLLFMYVQTKVTSSINFNKVVSFYSVVTPLNPLIYSLRNKEVKALGRVFSLNFWKGQ  
(SEQ ID NO: 221)

30 ATGCAACCATATACCAAAAACTGGACCCAGGTAACCTGAATTTGTCATGATGGGCTTTGCTG  
GCATCCATGAAGCACACCTCCTCTTCTTCATACTCTTCCTCACCATGTACCTGTTACCTTG  
GTGGAGAATTTGGCCATCATTTTAGTGGTGGGTTTGGACCACCGACTACGGAGACCCATGT  
ATTTCTTCCTGACACACTTGTCTGCCTTGAAATCTGGTACACTTCTGTTACAGTGCCCAAG  
ATGCTGGCTGGTTTTATTGGGGTGGATGGTGGCAAGAATATCTCTTATGCTGGTTGCCTAT  
CCCAGCTCTTCATCTTCACCTTTCTTGGGGCAACTGAGTGTTCCTACTGGCTGCCATGGCC  
35 TATGATCGTTATGTGGCCATTTGTATGCCTCTCCACTATGGGGCTTTTGTGTCCTGGGGCAC  
CTGCATCCGTCTGGCAGCTGCCTGTTGGCTGGTAGGTTTCCTCACACCCATCTTGCCAATCT  
ACCTCTTGTCTCAGCTAACATTTTGTGGCCCAAATGTCATTGACCATTCTCCTGTGATGCC  
TCACCTTGCTAGCCTTGTCTGCTCAGATGTCACTTGAAGGAGACTGTGGATTCTCTGG  
TGTCTCTGGCTGTGCTACTGGCCTCCTCTATGGTCATTGCTGTGTCTATGGCAACATCGTC  
40 TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCTTCTCTACCTGTGCAG  
CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTCTTTATGTATGTCCAGACCAAG  
GTGACCTCCTCCATCAACTTCAACAAGGTGGTATCTGTCTTCTACTCTGTTGTACGCCCAT  
GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTGAGTC  
TTTTCTCTCAACTTTTGAAGGGACAGTGA (SEQ ID NO: 222)

45

**AOLFR121 sequences:**

MKRKNFTEVSEFIFLGFSSFGKHQITLFVVFLTIVYILTLVANIIVTIICIDHHLHTPMYFFLSMLA  
SSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFFVILATNNCFLLTAMGYDRYVAICRPLRY  
TVIMSKGLCAQLVCGSFGIGLTMAVLHVTAMFNLPCGTVVDHFFCDIYPVMKLSCIDTTINEII  
50 NYGVSSSFVIFPIGLIFISYVLVISSILQIASAEGRKKTFCVSHLTVVIVHCGCASIAYLKPKSES  
SIEKDLVLSVTYTIITPLNPNVYSLRNKEVKDALCRVVGRNIS (SEQ ID NO: 223)

55 ATGAAGAGAAAGAACTTCACAGAAGTGTCAGAATTCATTTTCTTGGGATTTTCTAGCTTTG  
GAAAGCATCAGATAACCCTCTTTGTGGTTTCTCTAACTGTCTACATTTAACTCTGGTTGCT  
AACATCATCATTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATGTATTTCTT  
CCTAAGCATGCTGGCTAGTTCAGAGACGGTGTACACACTGGTCATTGTGCCACGAATGCTT

TTGAGCCTCATTTTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT  
 TTTTGTTATCTTGGCCACTAATAATTGCTTCCTGCTTACTGCAATGGGGTATGACCGCTATG  
 TGGCCATCTGCAGACCCCTGAGATACACTGTCATCATGAGCAAGGGACTATGTGCCAGCT  
 GGTGTGTGGGTCCTTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTTT  
 5 AATTTGCCGTTCTGTGGCACAGTGGTAGACCACTTCTTTTGTGACATTTACCCAGTCATGA  
 AACTTTCTTGCATTGATACCACTATCAATGAGATAATAAATTATGGTGTAAGTTTCAATTTGT  
 GATTTTGTGCCCATAGGCCTGATATTTATCTCCTATGTCCTTGTCTCTCTCCATCCTTC  
 AAATTGCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCACCTCACTGT  
 GGTATTGTCCACTGTGGCTGTGCCTCCATTGCCTACCTCAAGCCGAAGTCAGAAAGTTCA  
 10 ATAGAAAAAGACCTTGTTCTCTCAGTGACGTACACCATCATCACTCCCTTGCTGAACCTG  
 TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAA  
 ATATTTCTTAA (SEQ ID NO: 224)

**AOLFR122 sequences:**

15 MEWENQILVEFFLKGHSVHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL  
 SFLDICYTTTSIPSTLVSFLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMMAFDTRYVAICNPLR  
 YPIIMSKNAYVPMAGVSWFAGIVNSAVQTTFFVQLPFCRKNVINHFSCIELAVMKLACADISGN  
 EFLMLVATILFTLMPLLLIVISYSLISSLKIHSSSEGRSKAFSTCSAHLTVVIIFYGTILFMYMKPKS  
 20 KETLNSDDLDATDKIISMFGVMTMPMNPLIYSLRNKDVKEAVKHLPNRRFFSK (SEQ ID NO:  
 225)

ATGGAATGGGAAAACCAACCATTTCTGGTGGAATTTTTCTGAAGGGACATTCTGTTTACC  
 CAAGGCTTGAGTTACTCTTTTTGTGCTAATCTTCATAATGTATGGTTCATCCTTCTGGGG  
 AATGGTACTCTCATTTTAATCAGCATCTTGGACCTCACCTTCACACCCCTATGTACTTCTT  
 25 TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACACTAG  
 TGAGCTTCTTTTCAAGAAAGAACCATTTCTTTTCTGGCTGTGCAGTGCAGATGTTCTT  
 GGCTTGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTATG  
 TGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGCAAGAATGCCTATGTACCCAT  
 GGCTGTTGGGTCCTGGTTTGCAGGGATTGTCAACTCTGCAGTACAACTACATTTGTAGTA  
 30 CAATTGCCTTTCTGCAGGAAGAATGTCATCAATCATTTCTCATGTGAAATTCTAGCTGTCAT  
 GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCTCATGCTTGTGGCCACAATATTG  
 TTCACATTGATGCCACTGCTCTTGATAGTTATCTCTTACTCATTAAATCATTTCCAGCATCCT  
 CAAGATTCACTCCTCTGAGGGGAGAAGCAAAGCTTTCTCTACCTGCTCAGCCCATCTGACT  
 GTGGTCATAATATTCTATGGGACCATCTCTCATGTATATGAAGCCCAAGTCTAAAGAGA  
 35 CACTTAATTGATGACTTGGATGCTACCGACAAATTATATCCATGTTCTGTTGGGTGAT  
 GACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCAGT  
 AAAACACCTACCGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 226)

**AOLFR123 sequences:**

40 MYRFTDFDVSNISIYLNHVLFYTTQQAGDLEHMETRNYSAMTEFFLVGLSQYPELQLFLFLCL  
 IMYMIILLGNSLLIITILDSRLHTPMYFFLGNL SFLDICYTSSSIPMLIIFMSERKSISFIGCALQM  
 VVSLGLGSTECVLLAVMAYDHYVAICNPLRYSIIMNGVLYVQMAAWSWIIGCLTSLTQVLT  
 MMLPFCGNNVIDHITCEILALLKLVCSDITINVLTNTVSLVILLLLIFISYVILSSILRINCAE  
 GRKKAFSTCSAHSIVVILFYGSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPPIYSLRNKEV  
 45 KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

ATGTACAGATTTACAGATTTTGATGTATCAAACATTTCAATTTACCTGAATCATGTCCTTTT  
 CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT  
 GACTGAATTTCTTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTTCTGTTCTCTGC  
 50 TCTGCCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCATTATCATCACCATC  
 TTGGATTCTCGCCTCCATACTCCCATGTATTTCTTTCTTGGAAACCTCTCATTCTTGGACAT  
 CTGTTACACATCCTCATCCATTCTCCAATGCTTATTATATTTATGTCTGAGAGAAAATCCA  
 TCTCCTTCATTGGCTGTGCTCTGCAGATGGTTGTGTCCCTTGGCTTGGGCTCCACTGAGTGT  
 GTCCTCCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCACTGAGGTACT  
 55 CCATCATCATGAACGGAGTGCTGTATGTGCAAATGGCTGCATGGTCCTGGATCATAGGCTG  
 TCTGACCTCCCTATTGCAAACAGTTCTGACAATGATGTTGCCTTTCTGTGGGAATAATGTC

ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAAACTTGTTTGTTCAGATATCACCAT  
CAATGTGCTTATCATGACAGTGACAAATATTGTTTCACTGGTGATTCTTCTACTGTTAATTT  
TCATCTCCTATGTGTTTATTCTCTCTTCCATCCTGAGAATTAATTGTGCTGAGGGAAGAAAG  
AAAGCCTTCTCTACCTGTTTACGCGCACTCGATTGTGGTCATCTTATTCTACGGTTCAGCCCT  
5 TTTTATGTACATGAAACCCAAGTCAAAGAACACTAATACATCTGATGAGATTATTGGGCTG  
TCTTATGGAGTGGTAAGCCCAATGTTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG  
TCAAAGAGGCTGTAAAGAAAGTCTGAGCAGACATCTGCATTTATTGAAAATGTGA (SEQ  
ID NO: 228)

10 **AOLFR124 sequences:**

MNHSVVTEFIILGLTKKPELQGIIFLFLIVYLVAFLGNMLIIIAKIYNNTLHTPMYVFLTLAVV  
DICTTSIIPKMLGTMLTSENTISYAGCMSQLFLTWSLGAEMVLFTTMAYDRYVAICFPLHYST  
VMNHMCVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPPLALSCSPVRINEV  
MVYVADITLAIQDFILTCISYGFIIIVAILRIRTVGKRAKAFSTCSSHLTVVTLYYSPVIYTYIRPASS  
15 YTFERDKVVAALYTLVPTLNPVMVYSFQNRQEMQAGIRKVFAFLKH (SEQ ID NO: 229)

ATGAATCACAGCGTTGTAAGTGAAGTTCATTATTCTGGGCCTCACCAAAAAGCCTGAACTCC  
AGGGAATTATCTTCCTCTTTTTTCTCATTGTCTATCTTGTGGCTTTTCTCGGCAACATGCTC  
20 ATCATCATTGCCAAAATCTATAACAACACCTTGCATACGCCCATGTATGTTTCTCTTCTGAC  
ACTGGCTGTTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT  
GCTAACATCAGAAAATACCATTTCATATGCAGGCTGCATGTCCAGCTCTTCTTGTTCACA  
TGGTCTCTGGGAGCTGAGATGGTTCTCTTACCACCATGGCCTATGACCGCTATGTGGCCA  
TTTGTTCCTCTTTCATTACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC  
ATGGTCATGGCTATTGCAGTCACCAATTCCTGGGTGCACACAGCTCTTATCATGAGGTTGA  
25 CTTTCTGTGGGCCAAACACCATTGACCACTTCTTCTGTGAGATACCCCCATTGCTGGCTTTG  
TCCTGTAGCCCTGTAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCTGGCCA  
TAGGGGACTTTATTCTTACCTGCATCTCCTATGGTTTTATCATTGTTGCTATTCTCCGTATC  
CGCACAGTAGAAGGCAAGAGGAAGGCCTTCTCAACATGCTCATCTCATCTCACAGTGGTG  
ACCCTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATTGA  
30 AAGAGACAAGGTGGTAGCTGCACTCTATACTCTTGTGACTCCCACATTAAACCCGATGGTG  
TACAGCTTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTTCTGAAA  
CACTAG (SEQ ID NO: 230)

**AOLFR125 sequences:**

MTNQQTQMMEFLLVRFTENWVLLRLHALLFSLIYLTAVLMNLVILLMILDHRLHMAMYFFLRH  
LSFLDLCLISATVPKSIILNSVASTDSISFLGCVLQLFLVLLAGSEIGILTAMSYDRYAAICPLHC  
EAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSLNFYGSDELHQFFCDVPALLKLTCSKEHAI  
ISVSVAIGVCYAFSCLVCIVVSYYVIFSAVLRISQRQRQSKAFSNCVPHLIVVTVFLVTGAVAYL  
KPGSDAPSILDLLVSFVYSVAPPTLNPVIYCLKNKDIKSALS KVLWNVRSSGVMKDD (SEQ ID  
40 NO: 231)

ATGACCAATCAGACACAGATGATGGAATTCTTGCTTGTGAGATTTACTGAGAATTGGGTGC  
TCCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATTTA  
45 GTCATCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTAATTTTCTCTCCG  
ACATTTGTCCTTCTTAGACCTGTGTCTCATTCTGCCACAGTCCCCAAATCCATCCTCAACT  
CTGTCGCCTCCACTGACTCCATCTCCTTCTGGGGTGTGTGTTGCAGCTCTTCTTGGTGGTA  
CTGCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCTATGACCGCTATGCTGCCA  
TCTGCTGCCCCCTACACTGTGAGGCTGTCTGAGCAGAGGGCTCTGTGTCCAGTTGATGGC  
TCTGTCTCTGGCTCAACAGAGGGGCTTGGGACTCTTGTACACAGCTGGAACATTCTCTCTG  
50 AATTTTTATGGCTCTGATGAGCTACATCAGTTCTTCTGCGATGTCCCTGCCCTACTAAAGCT  
CACTTGTTCTAAAGAACATGCCATCATTAGTGTCACTGTGGCCATTGGGGTCTGTTATGCA  
TTTTCATGTTTAGTTTGCAATTGTAGTTTCTATGTGTACATTTCTCTGCTGTGTTAAGGAT  
ATCACAGAGACAGAGACAATCCAAAGCCTTTTCCAACCTGTGTGCCTCACCTCATGTTGTC  
ACTGTGTTTCTTGTAAACAGGTGCTGTTGCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT  
55 TCTAGACTTGCTGGTGTCTGTGTTCTATTCTGTGCGACCTCCAACCTTGAACCTGTTATCT

ACTGTCTGAAGAACAAGGACATTAAATCCGCTCTGAGTAAAGTCCTGTGGAATGTTAGAA  
GCAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

**AOLFR126 sequences:**

5 MFLYLCFIFQRTCSEEMEEENATLLTEFVLTGFLHQPDKIPLFLAFLVIYLITIMGNLGLIVLIW  
KDPHLHIPMYLFLGSLAFVDASLSSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL  
ATMAYDRYVAICKALLYPVIMTNELCIQLLVLSFIGGLLHALIHEAFSFRLTFCNSNIIQHIFYCDII  
PLLKISCTDSSINFLMVFI FAGSVQVFTIGTILISYTHILFTILEKKSIGIRKAVSTCGAHLLSVSLY  
10 YGPLTFKYLGSASPQADDQDMMESLFYTVIVPLLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID  
NO: 233)

ATGTTCCCTTTACCTTTGCTTCATTTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA  
ATGCAACATTGCTGACAGAGTTTGTTCACAGGATTTTTACATCAACCTGACTGTAAAAT  
ACCGCTCTTCCTGGCATTCTTGGAATATATCTCATCACCATCATGGGGAATCTTGGTCTAA  
15 TTGTTCTCATCTGGAAAGACCCTCACCTTCATATCCCAATGTACTTATTCCTTGGGAGTTTA  
GCCTTTGTGGATGCTTCGTTATCATCCACAGTGACTCCGAAGATGCTGATCAACTTCTTAG  
CTAAGAGTAAGATGATATCTCTCTCTGAATGCATGGTACAATTTTTTCCCTTGTAACCACT  
GTAACCACAGAATGTTTCTCTTGGAACAATGGCATATGATCGCTATGTAGCCATTTGCA  
AAGCTTTACTTTATCCAGTCATTATGACCAATGAACTATGCATTACAGCTATTAGTCTTGTC  
20 TTTATAGGTGGCCTTCTTCATGCTTTAATCCATGAAGCTTTTCATTACAGATTAACCTTCTG  
TAATTCCAACATAATAACAACCTTTTACTGTGACATTATCCATTGTTAAAGATTTCTGTGTA  
CTGATTCTCTATTAACCTTTCTAATGGTTTTTATTTTCGCAGGTTCTGTTCAAGTTTTTACCA  
TTGGAATCTCTATTAATCTTATACAAATTATCCTCTTTACAATCTTAGAAAAAGAAGTCTATC  
AAAGGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTATACT  
25 ATGGCCCCCTCACCTTCAAATATCTGGGCTCTGCATCTCCGCAAGCAGATGACCAAGATAT  
GATGGAGTCTCTATTTTACACTGTCATAGTTCCCTTTATTAAATCCCATGATCTACAGCCTGA  
GAAACAAGCAAGTAATAGCTTCATTCACAAAAATGTTCAAAAGCAATGTTTAG (SEQ ID  
NO: 234)

**AOLFR127 sequences:**

30 MSNEDMEQDNTLLTEFVLTGLTYQPEWKMPFLVFLVIYLITIVWNLGLIALIWNDPQLHIPM  
YFFLGSLAFVDAWISSTVTPKMLVNFLLAKNRMISLSECMIQFFSFAFGGTTECFLLATMAYDRY  
VAICKPLLYPVIMNNSLCIRLLAFSFLGGFLHALIHEVLIFRLTFCNSNIIHHFYCDIIPLMISCTD  
PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLLSVSLYYGPLIF  
35 MYLRPASQPADDQDMIDSVFYTHIPLNPIIYSLRNKQVIDSFTKMVKRNV (SEQ ID NO: 235)

ATGTCGAATGAGGACATGGAACAGGATAATACAACATTGCTGACAGAGTTTGTTCACAC  
GGACTTACATATCAGCCAGAGTGGAATAATGCCCTGTTCTTGGTGTTCTTGGTGATCTATC  
40 TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGGAATGACCCACAACCTTAC  
ATCCCCATGTACTTTTTCTTGGGAGTTTAGCCTTTGTTGATGCTTGGATATCTTCCACAGT  
AACTCCCAAAAATGTTGGTTAATTTCTTGGCCAAAAACAGGATGATATCTCTGTCTGAATGC  
ATGATTCAATTTTTTCTTTCATTTGGTGGAACTACAGAATGTTTTCTCTTGGCAACAAT  
GGCATATGATCGCTATGTAGCCATATGCAAACCTTTACTATATCCAGTGATTATGAACAAT  
45 TCACTATGCATACGGCTGTTAGCCTTCTCATTTTTAGGTGGCTTCTCCATGCCTTAATTCA  
TGAAGTCCTTATATTCAGATTAACCTTCTGCAATTCTAACATAATACATCATTTTTACTGTG  
ATATTATACCACTGTTTATGATTTCTGTACTGACCTTCTATTAATTTTCTAATGGTTTTTA  
TTTTGTCTGGCTCAATTCAGGTATTCACCATTTGTGACAGTTCTTAATTTCTTACACATTTGCT  
CTTTTCACAATCCTAAAAAAGAAGTCTGTTAGAGGCGTAAGGAAAGCCTTTTCCACCTGTG  
50 GAGCCCATCTCTTATCTGTCTCTTATATTATGGCCCACTTATCTTCATGTATTTGCGCCCT  
GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTTATACAATCATAATTC  
CTTTGCTAAATCCCATTATCTACAGCTCTGAGAAATAAACAAGTAATAGATTCAATCACAAA  
AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

**AOLFR128 sequences:**

55 METQNLTVVTEFILLGLTQSQDAQLLVFVLVLIIFYLIILPGNFLIIFTIKSDPGLTAPLYFFLGNLA  
LLDASYSFIVVPRMLVDFLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVMFAFDRYIAICRPLHY

STIMNPRACYALSLVLWLGFIHSIVQVALILHLPFCGPNQLDNFFCDVPQVIKLACTNTFVVEL  
LMVSNSSLGLLSLLCFLGLLASVAVILCRIREHSSEGKSKAISTCTTHIIIFLMFGPAIFIYTCPPQAFP  
ADKVVSFLHTVIFPLMNPVIYTLRNQEVKASMRKLLSQHMFC (SEQ ID NO: 237)

5 ATGGAAACACAGAACCTCACAGTGGTGACAGAATTCATTCTTCTTGGTCTGACCCAGTCTC  
AAGATGCTCAACTTCTGGTCTTTGTGCTAGTCTTAATTTTCTACCTTATCATCCTCCCTGGA  
AATTTCTCATCATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCTT  
TCTGGGCAACTTGGCCTTACTGGATGCATCCTACTCCTTCATTGTGGTTCCCAGGATGTTG  
GTGGACTTCCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTCAGCTCTTTT  
10 TCTTGCAATTTTCTTGGAGCGGGAGAGATGTTCTCCTCGTTGTGATGGCCTTTGACCGCTAC  
ATCGCCATCTGCCGGCCTTTACACTATTCAACCATCATGAACCCTAGAGCCTGCTATGCAT  
TATCGTTGGTTCTGTGGCTTGGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG  
CACTTGCCTTTCTGTGGCCCAAACCAAGTCGATAAATCTTCTGTGATGTTCCACAGGTCAT  
CAAGCTGGCCTGCACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCCAACAGTGGCCTG  
15 CTCAGCCTCCTGTGCTTCCTGGGCTTCTGGCCTCCTATGCAGTCATCCTCTGTGCTATAAG  
GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCCACATGCACCACCCATATTATCATT  
ATATTTCTCATGTTTGGACCTGCTATTTTCATCTACACTTGCCCCCTCCAGGCTTTCCAGC  
TGACAAGGTAGTTTCTCTTTTCCATACTGTCATCTTTCCTTTGATGAACCCTGTTATTTATA  
CGCTTCGCAACCAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTGT  
20 CTGA (SEQ ID NO: 238)

**AOLFR129 sequences:**

MALYFSLILHGMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLLFALFSVI  
YVVTVLGNLLIIVTVFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT  
25 QIFLLHLLGGVEMVLLVSMADFVVAICKPLHYMTIMNKKVCVLLVVTSWLLGLLHSGFQIPF  
AVNLPFCGPNVDSIFCDLPLVTKLACIDIYFVQVVIVANSGLSLSCFIILLISYSLILITIKNHSPT  
GQSKARSTLTAHITVVILFFGPCIFIYIWPFGNHSVDKFLAVFYTIITPILNPIIYTLRNKEMKISMK  
KLWRAVNSREDT (SEQ ID NO: 239)

30 ATGGCTCTTTATTTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTTCTCTACAGG  
TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAAACTATTAAATCAATCTCAAGTGC  
AGAATTCATTTTGCTGGGACTGACCAGCTCCCAGGATGTAGAGTTTCTTCTCTTTGCCCTCT  
TCTCGTTATCTATGTGGTCACAGTTTGGGTAACCTTCTTATTATAGTCACAGTGTTTAAAC  
ACCCCTAACCTGAATACTCCCATGTATTTCTCCTTGGAATCTCTCTTTTGTAGATATGAC  
35 CCTTGCTTCTTTTGCCACCCCTAAGGTGATTCTGAACTTGTTAAAAAAGCAGAAGGTAATT  
TCTTTTGCTGGGTGCTTCACTCAGATATTTCTCCTTCACTTACTGGGTGGGGTTGAAATGGT  
ACTGTTGGTCTCCATGGCTTTTGACAGATATGTGGCCATTTGTAAGCCCTACACTACATG  
ACCATCATGAACAAGAAGGTATGTGTTTGTCTGTAGTGACCTCATGGCTCTTGGGTCTCC  
TTCACTCAGGGTTTCAGATACCATTTGCTGTGAACCTTGCCCTTTTGTGGTCCCAATGTGGTA  
40 GACAGCATTTTGTGACCTCCCTTTGGTACTAAGCTTGCTGTATAGACATATATTTTGT  
ACAGGTAGTCATTGTTGCCAACAGTGGCATAATCTCCCTGAGCTGTTTCATTATTTTGTCTTA  
TCTCCTACAGTCTGATCCTCATAACCATTAAGAACCACTCTCCTACTGGGCAATCTAAAGC  
CCGTTCCACTTTGACTGCTCACATCACAGTGGTGATTCTCTTCTTTGGCCCATGCATCTTTA  
TCTACATTTGGCCCTTCGGCAACCACTCTGTAGATAAGTTCCTTGCTGTGTTTATACCATC  
45 ATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACAAAGAAATGAAGATATCCA  
TGAAAAAACTCTGGAGAGCTTTTGTGAATTCTAGAGAAGATACTTAG (SEQ ID NO: 240)

**AOLFR131 sequences:**

MASTSNVTELIPTGLFQDPAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS  
50 LVEISYSSTIAPKFIIDLLAKIKTISLEGCLTQIFFHFFGVAEILLIVVMA YDCYVAICKPLHYMNI  
ISRQLCHLLVAGSWLGGFCHSIIQILVIIQLPFCGPNVIDHYFCDLQPLFKLACTDTFMEGVIVLA  
NSGLFSVFSFLILVSSYIVILVNLRNHS AEGRHKALSTCASHITVVILFFGPAIFLYMRPSTFTED  
KLVAVFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)

55 ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG  
TGCAGAGTGTATGCTTTGTGGTGTTTCTCCCCGTGTACCTTGCCACGGTGGTGGGCAATGG

CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTTCCTTA  
 GCTGCCTGTCTTGGTGGAGATCAGTTATTCTCCACTATCGCCCCTAAATTCATCATAGAC  
 TTACTTGCCAAGATTAAAACCATCTCTCTGGAAGGCTGTCTGACTCAGATATTCTTCTTCCA  
 CTTCTTTGGGGTTGCTGAGATCCTTTTGATTGTGGTGATGGCCTATGATTGCTACGTGGCC  
 5 ATTTGCAAGCCTCTTCATTATATGAACATTATCAGTCGTCAACTGTGTCACTTCTGGTGGC  
 TGGTTCCTGGCTGGGGGGCTTTTGTCACTCCATAATTCAGATTCTCGTTATCATCCAATTGC  
 CTTCTGTGGTCCCAATGTGATTGACCACTATTTCTGTGACCTCCAGCCTTTATTCAAGCTT  
 GCCTGCACTGACACCTTCATGGAGGGGGTTATTGTGTTGGCCAACAGTGGATTATTCTCTG  
 TCTTCTCCTTCCTCATCTTGGTGTCTCTTATATTGTCATTCTGGTCAACTGAGGAACCAT  
 10 TCTGCAGAGGGGAGGCACAAAGCCCTCTCCACCTGTGCTTCTCACATCACAGTGGTCTATCT  
 TGTTTTTTGGACCTGCTATCTTCTCTACATGCGACCTTCTTCCACTTTCACTGAAGATAAA  
 CTTGTGGCTGTATTCTACACGGTCATCACCCCATGCTGAACCCCATCATTTACACACTCAG  
 GAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGGA  
 GGGAGTGA (SEQ ID NO: 242)

15

**AOLFR132 sequences:**

MVATNNVTEIIFVGFSGNQWSEQRVISVMFLMYTAVVLGNLIVVTILASKVLTSPMYFFLSYL  
 SFVEICYCSVMAPKLIFDSFIKRKVISLKGCLTQMFSLHFFGGTEAFLLMVMAYDRYVAICKPL  
 HYMAIMNQRMCGLLVRIAWGGGLLSVGGTFLIFQLPFCGPNIMDHYFCDVHPVLELACADT  
 20 PFISLLIITNGGSISVVSFFVLMASYLIILHFLRSHNLEGQHKALSTCASHVTVVDLFFIPCSLVYIR  
 PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCCAGAATTGGAGTG  
 AGCAGAGGGTCATTTCTGTGATGTTTCTCCTCATGTACACAGCTGTTGTGCTGGGCAATGG  
 25 CCTCATTGTGGTGACCATCCTGGCCAGCAAAGTGCTCACCTCCCCCATGTATTTCTTTCTCA  
 GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTCTATGGCCCCCAAGCTTATCTTTGAC  
 TCCTTTATCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTTCCCTCC  
 ATTTCTTTGGTGGCACTGAGGCCTTTCTCCTGATGGTGTATGGCCTATGACCGCTATGTGGC  
 CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAGCGAATGTGTGGTCTCCTCGTG  
 30 AGGATAGCATGGGGCGGGGGCCTGCTGCATTCTGTTGGGCAAACCTTCTGATTTTCCAGC  
 TCCCGTTCTGTGGCCCCAACATCATGGACCACTACTTCTGTGATGTCCACCCAGTGTGGA  
 GCTGGCCTGCGCAGACACCTTCTTCATTAGCCTGCTGATCATCACCAATGGCGGGCTCCATC  
 TCCGTAGTCAGTTTCTTCGTGCTGATGGCTTCTCACTGATCATCCTGCACCTTCTGAGAAG  
 CCACAACCTGGAGGGGAGCAGCACAAGGCCCTCTCCACCTGTGCCTCTCATGTACAGTTGTC  
 35 GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTACCCTCCCTGCAGA  
 CAAGATAGTTGCTGTATTTTATACAGTGGTCACACCTCTCTTAAACCCTGTGATTTACTCCT  
 TCAGGAATGCTGAAGTGAAAAATGCCATGAGGAGATTTATTGGGGGAAAAGTAATTTGA  
 (SEQ ID NO: 244)

40 **AOLFR133 sequences:**

MTEFIFLVLPNQEVQRVCFVIFLFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS  
 SATAPKLISDLLAERKVISWWGCMAQLFFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN  
 WQVCTVLVGIAWVGGFMHSFAQILLIFHLLFCGPNVINHYFCDLVPLLKLACSDTFLIGLLIVAN  
 GGTLISVISFGVLLASYMVILLHLRTWSSEGWCKALSTCGSHFAVVILFFGPCVFNSLRPSTTLPI  
 45 DKMVAVFYTVITAILNPVIYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

ATGACTGAATTCATTTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG  
 TGATATTTCTGTTCTTGTACACAGCAATTGTGCTGGGGAATTTCTCATTGTGCTCACTGTC  
 50 ATGACCAGCAGAAGCCTTGGTTCCCCCATGTACTTCTTCTCAGCTACCTCTCCTTCATGGA  
 GATCTGCTACTCCTCCGCTACAGCCCCCAAACCTCATCTCAGATCTGCTGGCTGAAAGGAAA  
 GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTTCTTGCACCTCTTTGGTGGCACTGA  
 GATTTTCTGCTCACTGTGATGGCCTATGACCACTATGTGGCCATCTGCAAGCCCCTCAGC  
 TACACCACCATCATGAAGTGGCAGGTGTGTAAGTGTGCTTGTAGGAATAGCATGGGTGGGA  
 GGCTTCATGCATTCTTTGCACAAATCCTTCTCATCTTCCACCTGCTCTTCTGTGGCCCCAA  
 55 TGTGATCAATCACTATTTCTGTGACCTAGTTCCCTTCTCAAACCTTGCTGCTGACACCT  
 TCCTCATTGGTCTGCTGATTGTTGCCAATGGAGGCACCTGTCTGTGATCAGTTTTGGGGT

CCTCTTAGCATCCTATATGGTCATCTTGCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG  
 TGCAAAGCCCTCTCCACCTGTGGGTCCCATTTTCGCTGTGGTTATCTTGTCTTTGGGCCCTG  
 CGTCTTCAACTCTCTGAGGCCTTCTACCACTCTGCCCATAGACAAGATGGTGGCTGTGTCT  
 ACACAGTGATAACCGCGATCCTGAACCTGTCTACTCTCTGAGAAATGCTGAAATGAG  
 5 GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID  
 NO: 246)

**AOLFR134 sequences:**

MTTIILEVDNHTVTTRFILLGFTRPAFQLFFSIFLATYLLTLENLLILAIHSDGQLHKPMYFFL  
 10 SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC  
 NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFLAQLHYCGMPQINHIFCDISPLLNVSCE  
 DASQAEMVDFFLALMVIAIPLCVVVASAAILATILRIPSAQGRQKAFSTCASHLTVVILFYSM  
 LFTYARPKLMYAYNSNKVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTIHCRGSGPQNGAFS  
 S (SEQ ID NO: 247)

15 ATGACCACCATAATTCTGGAAGTAGATAATCATACAGTGACAACACGTTTCATTCTTCTGG  
 GGTTTCCAACACGACCAGCCTTCCAGCTTCTCTTTTCTCCATTTTCCTGGCAACCTATCTG  
 CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA  
 AGCCCATGTACTTCTTCTTGAGCCACCTCTCCTTCCCTGGAGATGTGGTATGTCACAGTCATC  
 20 AGCCCCAAGATGCTTGTGACTTCCTCAGTCATGACAAGAGTATTCCTTCAATGGCTGCA  
 TGACTCAACTTACTTTTTGTGACCTTTGTCTGCACTGAGTACATCCTTCTTGCTATCATG  
 GCCTTTGACCGCTATGTAGCCATTGTAATCCACTACGCTACCCAGTCATCATGACCAACC  
 AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTTCTGTGGACTCATGACTGCCATGATTAA  
 GATGGTTTTTATAGCAAACTTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTGTG  
 25 ATATCTCTCCACTCCTTAACGTCTCCTGTGAGGATGCCTCACAGGCTGAGATGGTGGACTT  
 CTTCTTGCCCTCATGGTCATTGCTATTCCTCTTTGTGTTGTGGTGGCATCCTACGCTGCTA  
 TCCTTGCCACCATCCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTCTCCACCTG  
 TGCCTCCACCTGACCGTCGTAATTCTCTTCTATTCCATGACACTTTTCACCTATGCCCGTC  
 CCAAACCTCATGTATGCCTACAAATCCAACAAAGTGGTATCTGTTCTCTACACTGTCATTGTT  
 30 CCACTCCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA  
 AGACCATAATTGCAGAGGAAGTGGGCCCCAGGGAAATGGGGCTTTCAGTAGTTAA (SEQ  
 ID NO: 248)

**AOLFR135 sequences:**

35 MIFPSHDSQAFSTVDMEVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILIRT  
 DSHLHTPMYFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL  
 AAMAYDRHAAICNPLLYSGTMSTALCTGLVAGSYIGGFLNAIAHTANTFRLHFCGKNIDHFFC  
 DAPPLVKMSCTNTRVYEKVLGTVGFTVLSSILAILISYVNILLAILRIHSASGRHKAFSTCASHL  
 ISVMLFYGSLLFMYSRPSSTYSLERDKVAALFYTVINPLLNPLIYSLRNKDIKEAFRKATQTIQPP  
 40 T (SEQ ID NO: 249)

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTCACCTCCGTGGACATGGAAGTGGGAAATT  
 GCACCATCCTGACTGAATTCATCTTGTGGGTTTCTCAGCAGATTCCCAGTGGCAGCCGAT  
 TCTATTTGGAGTGTTTCTGATGCTCTATTTGATAACCTTGTGAGGAAACATGACCTTGGTTA  
 45 TCTTAATCCGAACCTGATTCCCACTTGATACACCTATGTACTTTTTCATTGGCAATCTGTCT  
 TTTTGGATTCTGGTATACCTCTGTGTATACCCCCAAAATCCTGGCCAGTTGTGTCTCAGA  
 AGATAAGCGCATTTCTTGGCTGGATGTGGGGCTCAGCTGTTTTTTCTGTGTTGTAGCCT  
 ACACTGAATGCTATCTCCTGGCAGCCATGGCATATGACCGCCATGCAGCAATTTGTAACCC  
 ATTGCTTTATTGAGTACCATGTCCACCGCCCTCTGTACTGGGCTTGTGCTGGCTCCTACA  
 50 TAGGAGGATTTTGAATGCCATAGCCATACTGCCAATACATTCCGCCTGCATTTTGTGG  
 TAAAAATATCATTGACCACTTTTCTGTGATGCACCACCATTGGTAAAAATGTCCTGTACA  
 AACACCAGGGTCTACGAAAAAGTCTGCTTGGTGTGGTGGGCTTCACAGTACTCTCCAGCA  
 TTCTTGCTATCCTGATTTCTATGTCAACATCCTCCTGGCTATCCTGAGAATCCACTCAGCT  
 TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCACCTCATCTCAGTCATGCTCTTCTA  
 55 TGGATCATTGTTGTTTATGTATTCAAGGCCTAGTTCACCTACTCCCTAGAGAGGGACAAA  
 GTAGCTGCTCTGTTCTACACCGTGATCAACCCACTGCTCAACCCCTCTCATCTATAGCCTGAG

AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG  
A (SEQ ID NO: 250)

**AOLFR136 sequences:**

5 MTMENYSMAAQFVLDGLTQQAELQLPLFLLFLGIYVVTVVGNLGMILLIAVSPLLHTPMYYFL  
SSLSFVDFCYSSVITPKMLVNFLGKKNTILYSECMVQLFFFVVFVVAEGYLLTAMAYDRYVAIC  
SPLLYNAIMSSWVCSLLVLAAFFLGFLSALHTSAMMKLSFCKSHIINHIFCDVLPLLNLSCSNT  
HLNELLLFIAGFNTLVPTLAVAVSYAFILYSILHIRSSEGRSKAFGTCCSHLMNAVVIFFGSITFMY  
FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)

10 ATGACCATGGAAAATTATTCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAAACACAGCAAG  
CAGAGCTCCAGCTGCCCTCTCCTCCTGTTCTGGAATCTATGTGGTCACAGTAGTGGG  
CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTCTACTTCACACCCCCATGTACTATT  
TCCTCAGCAGCTTGTCTTCGTCGATTCTGTCTATTCTCTGTCTATTCTCCCAAAATGCTG  
15 GTGAACTTCCTAGGAAAGAAGAATACAATCCTTTACTCTGAGTGCATGGTCCAGCTCTTTT  
TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCCTGACTGCCATGGCATATGATCGCTA  
TGTTGCCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCCTCATGGGTCTGCTCACTGC  
TAGTGCTGGCTGCCTTCTTCTTGGGCTTTCTCTCTGCCTTGACTCATACAAGTGCCATGATG  
AACTGTCTTTTGCAAATCCCACATTATCAACCATTACTTCTGTGATGTTCTTCCCTCCT  
20 CAATCTCTCCTGCTCCAACACACACCTCAATGAGCTTCTACTTTTTATCATTGCGGGGTTTA  
ACACCTTGGTGCCCAACCTAGCTGTTGCTGTCTCCTATGCCTTCATCCTCTACAGCATCCTT  
CACATCCGCTCCTCAGAGGGCCGGTCCAAAGCTTTTGGAACATGCAGCTCTCATCTCATGCT  
CTGTGGTGATCTTCTTTGGGTCCATTACCTTCATGTATTTCAAGCCCCCTTCAAGTAACTCC  
CTGGACCAGGAGAAGGTGTCTCTGTGTTCTACACCACGGTGATCCCCATGGAACCTT  
25 TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAAGGAAGGTCTTAGTAGGAA  
AATGA (SEQ ID NO: 252)

**AOLFR137 sequences:**

MSPENQSSVSEFLLLGLPIRPEQQAVFFALFLGMYLTTVLGNLLIMLLIQLDLHPTMYFFLSH  
30 LALTDISFSSVTPKMLNMNMQTHLAVFYKGCISQTYFFIFFADLDSFLITSMAYDRYVAICHPL  
HYATIMTQSQVMLVAGSWVIACACALLHTLLLAQLSFCADHIIPHYFCDLGALLKLSGSDTSL  
NQLAIFTAALTAIMLPFLCILVSYGHIGVTILQIPSTKGICKALSTCGSHLSVVTIYYRTIIGLYFLP  
PSSNTNDKNIIASVIYTAVTPLNPFYISLRNKDIKGALRKLLSRGAVAHACNLSTLGG (SEQ  
ID NO: 253)

35 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTCCTGGGCCTCCCCATCCGGC  
CAGAGCAGCAGGCCGTGTTCTTCGCCCTGTTCTGCGCATGTACCTGACCACGGTGCTGGG  
GAACCTGCTCATCATGCTGCTCATCCAGCTAGACTCTCACCTTCACACCCCCATGTACTTCT  
TCCTTAGCCACTTGGCCCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG  
40 ATGAACATGCAGACTCAGCACCTAGCCGTCTTTACAAGGGATGCATTTACAGACATATT  
TTTTCATATTTTTTGTGACTTAGACAGTTTCTTATCACTTCAATGGCATATGACAGGTAT  
GTGGCCATCTGTATCCTCTACATTATGCCACCATCATGACTCAGAGCCAGTGTGTCATGC  
TGGTGGCTGGGTCTGGGTCTGTCGCTTGTGCGTGTGCTCTTTTGATACCCCTCCTCCTGGCC  
CAGCTTTCTTCTGTGCTGACCACATCATCCCTCACTACTTCTGTGACCTTGGTGCCCTGCT  
45 CAAGTTGTCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA  
GCCATTATGCTTCCATTCTGTGATCCTGCTGTTCTTATGGTCACATTGGGGTCCACCTCCT  
CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTTGTCCACTTGTGGATCCCACCTCTCA  
GTGGTGACTATCTATTATCGGACAATTATTGGTCTCTATTTTCTTCCCCCATCCAGCAACAC  
CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA  
50 TTCATTTACAGTCTGAGAAATAAAGACATTAAGGGAGCCCTAAGAAAACCTCTGAGTAGG  
TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

**AOLFR138 sequences:**

MLNFTDVTEFILLGLTSRREWQVLFFVFLVYIITVVGNIGMMLLIKVSPQLNSPMYFFLSHLS  
55 FVDVWFSSNVTPKMLENLFSDDKKTISYADCLAQCCFFIALVHVEIFILAAIAFDRTYVIGNPLLY  
GSKMSRGVCIRLITFPYIYGFLTSLTATLWTYGLYFCGKIEINHFCADPPLIKMACAGTFVKEY



TMLILAGINFTYSLTVIIISYLFILIAILMRSAEGRQKAFSTCGSHPTAVIIFYGTLIFMYLRRPTE  
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

5 ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGGAAT  
GGCAAGTTCTCTTCTTCATCGTTTTTCTTGTTGCTACATTATCACCGTGGTGGCAATATC  
GGCATGATGTTGTTAATCAAGGTCAGTCCTCAGCTTAACAGCCCCATGTACTTTTTCTCA  
GTCATTGTCAATTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAAAAT  
CTGTTATCAGATAAAAAACAATTTCTTATGCTGGCTGTTTAGCACAGTGTTCCTTCTTCAT  
TGCTCTTGTCCATGTGGAAATTTTATTCTTGCTGCGATTGCCTTTGATAGATACACAGTGA  
10 TTGGAAATCCTTTGCTTTATGGCAGCAAAATGTCAAGGGATGTCTGTATTGCGACTGATTAC  
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTTGT  
ACTTCTGTGGAAAAATTGAGATCAACCATTCTACTGTGCAGATCCACCTCTCATAAAAAT  
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGCTCATACTTGCCGGCATCAACTTC  
ACATATTCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT  
15 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCCTGACAGCTGT  
CATCATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCCACAGAGGAGTCTGTG  
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA  
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT  
GTAA (SEQ ID NO: 256)

20

**AOLFR139 sequences:**

MGFPGIHSWQHWSLPLALLYLLALSANILILINKEAALHQPMMYFLGILAMADIGLATTIMP  
KILAILWFNAKTISLLECFAQMYAIHCFVAMESSTFVCMADRYVAICRPLRYPSTITESFVKAN  
GFMALRNSLCLISVPLLAQRHYCSQNQIEHCLCSNLGVTSLSCDDRRINSINQVLLAWTLMGS  
25 DLGLILSYALILYSVLKLNPEAASKALSTCTSHLILFFYTVIIVISITRSTGMRVPLIPVLLNVL  
HNVIPPALNPMVYALKNKELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

30 ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCCTGGCTCTGCTCT  
ACCTCTTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGCAGCACT  
GCACCAGCCTATGTACTATTTCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTACC  
ACCATCATGCCTAAGATTTTGGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG  
AGTGCTTTGCTCAGATGTATGCCATACATTGCTTTGTGGCCATGGAATCAAGTACCTTTGT  
CTGCATGGCTATTGATAGATATGTAGCCATTTGTGCGACCGCTACGATATCCATCAATCATC  
ACTGAATCTTTGTTTTCAAAGCAAATGGGTTTCATGGCACTGAGAAACAGCCTGTGTCTCA  
35 TCTCAGTGCCTCTGTTGGCTGCCAGAGGCATTACTGCTCCCAGAAATCAAATTGAGCACTG  
TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCATT  
AACCAGGTCCTTTTGGCTTGGACACTCATGGGAAGTGACCTGGGTTTGATTATTTATCAT  
ATGCTCTAATACTTTACTCTGTCTGAAGCTGAAGCTCTCCAGAAGCTGCATCCAAGGCCTT  
AAGTACCTGCACCTCCACCTCATCTTAATCCTTTTCTTCTACACAGTCATCATTTGTGATTT  
40 CCATTACTCGTAGTACAGGAATGAGAGTTCCCTTATTCCAGTTCTACTTAATGTGCTACA  
CAATGTCAATTCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAGGAATCAGG  
CAAGGCTTATACAAGGTAAGTACTTAGACTGGGAGTGAAGGGCACCTGA (SEQ ID NO: 258)

**AOLFR140 sequences:**

45 MLTLNKTDLIPASFILNGVPGLEDLQLWISFPFCSMYVAMVGNCGLLYLIHYEDALHKPMY  
FLAMLSFTDLVMCSSTIPKALCIFWHLKDIFDECLVQMFFIHTFTGMESGVLMLMALDRYV  
AICYPLRYSTILNPNVIAKVGTATFLRGVLLIIPFTFLTKRLPYCRGNILPHTYCDHMSVAKLSCG  
NVKVNAYGLMVALLIGGFILCTISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAF  
FSFFSHRFGEHIIPPSCHIIIVANIYLLLPPTMNPVYGVKTKQIRDCVIRILSGSKDTKSYSM (SEQ  
50 ID NO: 259)

55 ATGCTAACACTGAATAAAACAGACCTAATACCAGCTTCATTTATTCTGAATGGAGTCCAG  
GACTGGAAGACACACAACCTCTGGATTTCTTCCCATTCTGCTCTATGTATGTTGTGGCTAT  
GGTAGGGAATTGTGGACTCCTCTACCTCATTCACTATGAGGATGCCCTGCACAAACCCATG  
TACTACTTCTTGGCCATGCTTTCTTTACTGACCTTGTTATGTGCTCTAGTACAATCCCTAA  
AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTTGATGAATGCCTTGTCCAG

ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGCTTATGCTTATGGCCCTGG  
 ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTCACCAATCCTGTAATT  
 GCAAAGGTTGGGACTGCCACCTTCTGAGAGGGGTATTACTCATTATTCCCTTTACTTTCCT  
 CACCAAGCGCCTGCCCTACTGCAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG  
 5 TCTGTAGCCAAATTGTCCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG  
 CCCTCCTGATTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCTCCGG  
 GCAGTGGTCAGCCTCTCCTCAGCAGATGCTCGGCAGAAGGCCTTTAATACCTGCACTGCCC  
 ACATTTGTGCCATTGTTTTCTCCTATACTCCAGCTTTCTTCTCCTTCTTTTCCCACCGCTTTG  
 GGAACACATAATCCCCCTTCTTGCCACATCATTGTAGCCAATATTATCTGCTCCTACCA  
 10 CCCACTATGAACCTATTGTCTATGGGGTGAACCAACAGATACGAGACTGTGTCATAA  
 GGATCCTTTCAGGTTCTAAGGATACCAATCCTACAGCATGTGA (SEQ ID NO: 260)

**AOLFR141 sequences:**

MSSTLGHNMESPNHTDVPDPSVFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVL  
 15 HKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHAFCMMESTVLLAM  
 AFDRYVAICHPLRYATILDTIAHIGVAAVVRGSLMLPCPFLIGRLNFCQSHVILHTYCEHMA  
 VVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVC  
 VILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLPPLNPNVYGVKTKQIRKRVVRVFSQSGQ  
 GMGIKASE (SEQ ID NO: 261)

20 ATGTCCAGCACTCTTGGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCTTCTG  
 TCTTCTCTCCTGCGCATCCCAGGTCTGGAACAATTCATTGTGGCTCTCACTCCCTGTG  
 TGTGGCTTAGGCACAGCCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTG  
 AACCAGTCTTGACAAGCCTGTGTACCTTTTTCTGTGCATGCTCTCAACCATCGACTTGGCT  
 25 GCCTCTGTCTCCACAGTTCCCAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT  
 CTGCCTCTGCCTGCCTGGCACAGATGTTCTTCATTGCTGCTTCTGCATGATGGAGTCCACT  
 GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA  
 CAATCCTCACTGACACCATCATTGCCACATAGGGGTGGCAGCTGTAGTGCGAGGCTCCCT  
 GCTCATGCTCCCATGTCCCTTCCTTATTGGGCGTTTGAACCTCTGCCAAAGCCATGTGATCC  
 30 TACACACGTACTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGAGACACCAGGCCTA  
 ACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCATTGGGGTTGACTTGTTTTGCAATTGG  
 TCTCTCCTATGCCCTAAGTGACAAGCTGTCTTCTGCCTCTCATCCCATGAAGCTCGGTCCA  
 AGGCCCTAGGACCTGTGGTTCCCATGTCTGTGTCATCCTCATCTCTTATACACCAGCCCTC  
 TTCTCCTTTTTTACACACCGCTTTGGCCATCAGGTTCCAGTCCATATTACATTCTTTTGGC  
 35 CAATGTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAAAC  
 AGATCCGTAAAAGAGTTGTGAGGGTGTTCAAAGTGGGCAGGGAATGGGCATCAAGGCAT  
 CTGAGTGA (SEQ ID NO: 262)

**AOLFR143 sequences:**

40 MLGLNGTPFPQATLQLTGIPGIQTGLTWVALIFCILYMISIVGNLSILTLVFWEPALHQPMMYYFL  
 SMLALNDLGVSFSTLPTVISTFCFNYNHVAFAACLVQMFFIHTFSFMESGILLAMSLDRFVAICY  
 PLRYVTVLTHNRILAMGLGILTKSFTTLFPFPVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI  
 HVNNIYGLLVIIFTYGMDSFILLSYALILRAMLVISQEQRLKALNTCMSHICAVLAFYVPIIAVS  
 MIHRFWKSAPPVVHVMMSNVYLFVPPMLNPIIYSVKTKAIRKGILKFFHKSQA (SEQ ID NO:  
 45 263)

ATGCTGGGTCTCAATGGCACCCCTTCCAGCCAGCAACACTCCAGCTGACAGGCATTCCCTG  
 GGATACAAACAGGCCTCACCTGGGTTGCCCTGATTTTCTGCATCCTCTACATGATCTCCATT  
 GTAGGTAACCTCAGCATTCTCACTCTGGTGTGTTTGGGAGCCTGCTCTGCATCAGCCCATGT  
 50 ACTACTTCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCTTTTCTACACTTCCCACT  
 GTGATTTCTACTTTCTGCTTCAACTACAACCATGTTGCGTTTAAATGCTTGCCTGGTCCAGAT  
 GTTCTTCATCCACACTTTCTCCTTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC  
 GCTTTGTGGCTATTTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG  
 GCTATGGGTCTGGGCATCCTTACCAAGAGTTTACCACCTCTCTTCCCTTTCCCTTTTGTGGT  
 55 GAAACGACTGCCCTTCTGCAAAGGCAATGTTTTGCATCACTCCTACTGTCTCCATCCAGAT  
 CTCATGAAAGTAGCATGTGGAGACATCCATGTAAACAACATTATGGGCTCTTGGTGATCA

TTTTACCTATGGTATGGACTCAACTTTCATCCTGCTTTCCTACGCATTGATCCTGAGAGCC  
 ATGCTGGTCATCATATCCCAGGAACAGCGGCTCAAGGCACTCAACACCTGCATGTCACACA  
 TCTGTGCAGTGCTGGCCTTTTATGTGCCATAATTGCTGTCTCCATGATTCACCGCTTCTGG  
 AAAAGTGCTCCACCTGTTGTTCATGTCATGATGTCCAATGTCTACCTGTTTGTACCACCCAT  
 5 GCTCAACCTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTC  
 TTCCATAAATCCCAGGCCTGA (SEQ ID NO: 264)

**AOLFR144 sequences:**

MGLFNVTHPAFFLLTGIPGLESSHWSLGPVCVMAVALGGNTVILQAVRVEPSLHEPMMYYFL  
 10 SMLSFSVDVAISMATLPTVLRFTCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDYVAICD  
 PLRYATVLTTEVIAAMGLGAAARSFITLFLPFLIKRLPICRSNVLSHSYCLHPDMMRLACADISI  
 NSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS  
 TVHRFGKHVPCYIHLMSNVYLFVPPVLNPLIYSAKTKEIRRAIFRMFHHIKI (SEQ ID NO: 265)

ATGGGGTTGTTCAATGTCACTCACCTGCATTCTTCCTCCTGACTGGTATCCCTGGTCTGGA  
 GAGCTCTCACTCCTGGCTGTCAGGGCCCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA  
 AATACAGTGATCCTGCAGGCTGTGCGAGTGGAGCCCAGCCTCCATGAGCCCATGTACTACT  
 TCCTGTCCATGTTGTCTTCAGTGATGTGGCCATATCCATGGCCACACTGCCCACTGTACTC  
 CGAACCTTCTGCCTCAATGCCCCGAACATCACTTTTGATGCCTGTCTAATTCAGATGTTTCT  
 20 TATTCACCTTCTTCCATGATGGAATCAGGTATTCTGCTGGCCATGAGTTTGACCGCTATG  
 TGGCCATTTGTGACCCCTTGCCTATGCAACTGTGCTCACCCTGAAGTCATTGCTGCAAT  
 GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCTTTTCCCTCTTCCCTTTCTTATTAAGA  
 GGCTGCCTATCTGCAGATCCAATGTTCTTCTCACTCCTACTGCCTGCACCCAGACATGATG  
 AGGCTTGCCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTGTCTTGTATCCAC  
 25 CTTTGGCATGGACCTGTTTTTATCTTCTCCTCTCCTATGTGCTCATTCTGCGTTCTGTATGG  
 CCACTGCTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTACATATCCTGGC  
 TGTACTTGCATTTTATGTGCAATGATTGGGGTCTCCACAGTGCACCGCTTTGGGAAGCAT  
 GTCCCATGCTACATACATGTCTCATGTCAAATGTGTACCTATTTGTGCTCCTGTGCTCAA  
 CCCTCTCATTTATAGCGCCAAGACAAAGGAAATCCGCCGAGCCATTTCCGCATGTTTCAC  
 30 CACATCAAAATATGA (SEQ ID NO: 266)

**AOLFR145 sequences:**

MSVQYSLSPQFMLLSNITQFSPIFYLTSPFGLGKHWIFIPFFFMVMVAISGNCFILIIKTNPRLH  
 TPMYYLLSLLALTDLGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCIHSFSMESSVLLMMSFD  
 35 RFVAICHPLRYSVIITGQQVVRAGLIVFRGPVATIPIVLLLKAFPYCGSVVLSHSFCLHQEVIQLA  
 CDTTFNPLYGLMVVFTVMLDLVLIALSYGLILHTVAGLASQEEQRRAFQTCTAHLCAVLVF  
 FVPMMLSLVHRFGKHAPPAIHLMLANVYLFVPPMLNPIIYSIKTKEIHRAIKLLGLKKASK  
 (SEQ ID NO: 267)

ATGTCAGTCCAATATTCGCTCAGTCTCAATTCATGCTGCTATCCAACATTACTCAGTTTAG  
 CCCCATATTCTATCTCACCAGCTTTCCTGGATTGGAAGGCATCAAACACTGGATTTTCATCC  
 CCTTTTCTTTATGTACATGGTTGCCATCTCAGGCAATTGTTTCATTCTGATCATTATTAAG  
 ACCAACCTCGTCTGCACACACCCATGTACTATCTACTATCCTTGCTGGCCCTCACTGACCT  
 GGGGCTGTGTGTGTCCACGTTGCCACCACTATGGGGATCTTCTGGTTTAACTCCCAGAGT  
 45 ATCTACTTTGGAGCGTGTCAAATCCAGATGTTCTGCATCCACTCTTTTCTCTCATGGAGTC  
 CTCAGTGCTCCTCATGATGTCTTTGACCGCTTTGTGGCCATCTGCCACCTCTGAGGTATT  
 CGGTCAATTATCACTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTCATCTTCCGGGGACC  
 TGTGGCCACTATCCCTATTGTCTCCTCCTGAAGGCTTTTCCCTACTGTGGATCTGTGGTCC  
 TCTCCCACTCATTTTGCCTGCACCAGGAAGTGATACAGCTGGCCTGCACAGATACCACCTT  
 50 CAATAATCTGTATGGACTGATGGTGGTAGTTTCACTGTGATGCTGGACCTGGTGCTCATC  
 GCACTGTCCTATGGACTCATCTGCACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC  
 GCCGTGCCCTTTCAGACATGCACCGCTCATCTCTGTGCTGTGCTAGTATCTTTGTGCCCATG  
 ATGGGGCTGTCCCTGGTGCACCGTTTTTGGGAAGCATGCCCCACCTGCTATTCATCTTCTTAT  
 GGCCAATGTCTACCTTTTTGTGCTCCCATGCTTAACCAATCATATACAGCATTAAAGACC  
 55 AAGGAGATCCACCGTGCCATTATCAAACCTCCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ  
 ID NO: 268)

**AOLFR146 sequences:**

MSQVTNTTQEGIFYLTDIPGFEASHIWISIPVCCLYTISIMGNTTILTVIRTEPSVHQRMVFLSM  
LALTDLGLTLTTLPTVMQLLWFNVRRISSEACFAQFFFLHGFSFMESSVLLAMSVDYVAICCP  
5 LHYASILTNEVIGRTGLAIICCCVLAVLPSLFLKRLPFCHSHLLSRSYCLHQDMIRLVCADIRLN  
SWYGFALALLIIVDPLLVISYTLILKNILGTATWAERLRALNNCLSHILAVLVLYIPMVGVSMT  
HRAKHASPLVHVIMANIYLLAPPVMNPIIYSVKNKQIQWGMLNFLSLKNMHSR (SEQ ID NO:  
269)

10 ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG  
GATTTGAGGCCTCCCACATCTGGATCTCCATCCCCGTCTGCTGTCTCTACACCATCTCCATC  
ATGGGCAATACCACCATCCTCACTGTCTCGCACAGAGCCATCTGTCCACCAGCGCATGT  
ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCTCACCACCCTACCCACA  
GTCATGCAGCTTCTCTGGTTCAACGTTCTGATAGAATCAGCTCTGAGGCCTGTTTTGCTCAGTT  
15 TTTCTTCCTTCATGGATTCTCCTTTATGGAGTCTTCTGTCCTCCTGGCTATGTCCGTTGACT  
GCTATGTGGCCATCTGCTGTCCCCCTCCATTATGCCTCCATCCTCACCAATGAAGTCATTGGT  
AGAACTGGGTTAGCCATCATTTGCTGCTGTGTTCTGGCGGTTCTTCCCTCCCTTTTCTTACT  
CAAGCGACTGCCTTTCTGCCACTCCCACCTTCTCTCTCGCTCCTATTGCCTCCACCAGGATA  
TGATCCGCCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTGCTCTTGCCTT  
20 GCTCATTATTATCGTGGATCCTCTGCTCATTGTGATCTCTATACACTTATTCTGAAAAATA  
TCTTGGGCACAGCCACCTGGGCTGAGCGACTCCGTGCCCTCAATAACTGCTGCTCCACAT  
TCTAGCTGTCTGGTCTCTACATTCCCATGGTTGGTGTATCTATGACTCATCGCTTTGCCA  
AGCATGCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCACCCCCGGT  
GATGAACCCCATCATTTACAGTGTAAGAACAAGCAGATCCAATGGGGAATGTAAATTC  
25 CTTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

**AOLFR147 sequences:**

MPSASAMIIIFNLSSYNPGPFILVGIPGLEQFHVWIGIPFCIIYIVAVVGNICILLYLIVVEHSLHEPMP  
FFLSMLAMTDLILSTAGVPKALSIFWLGAAREITFPGLTQMFFLHYNFVLDSAILMAMAFDHVY  
30 AICSPLRYTTILTPKTIKSAMGISFRSFCILPDVFLLTCLPFCRTRIIPHTYCEHIGVAQLACADISI  
NFWYGFCVPIMTVISDVILIAVSYAHILCAVFLGPSQDACQKALGTGSHVCVILMFYTPAFFSI  
LAHRFGHNVSRTFHIMFANLYIVIPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO:  
271)

35 ATGCCATCTGCCTCTGCCATGATCATTTTCAACCTGAGCAGTTACAATCCAGGACCCCTTCAT  
TCTGGTAGGGATCCCAGGCCTGGAGCAATCCATGTGTGGATTGGAATTCCTTCTGTATC  
ATCTACATTGTAGCTGTTGTGGGAACTGCATCCTTCTCTACCTCATTGTGGTGGAGCATA  
GTCTTCATGAACCCATGTTCTTCTTCTCTCCATGCTGGCCATGACTGACCTCATCTTGTCC  
ACAGCTGGTGTGCCTAAAGCACTCAGTATCTTTGGCTAGGGGCTCGCGAAATCACATTCC  
40 CAGGATGCCTTACACAAATGTTCTTCCCTTCACTATAACTTTGTCTGGATTGAGCCATTCTG  
ATGGCCATGGCATTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATACCACCATCTT  
GACTCCCAAGACCATCATCAAGAGTGCTATGGGCATCTCCTTTCGAAGCTTCTGCATCATC  
CTGCCAGATGTATTCTTGCTGACATGCCTGCCTTCTGCAGGACACGCATCATACCCACA  
CATACTGTGAGCATATAGGTGTTGCCAGCTCGCCTGTGCTGATATCTCCATCAACTCTG  
45 GTATGGCTTTTGTGTTCCCATCATGACGGTCATCTCAGATGTGATTCTCATTGTCTGTTTCCT  
ACGCACACATCCTCTGTGCTGTCTTTGGCCTTCCCTCCCAAGATGCCTGCCAGAAAGCCCT  
CGGCACTTGTGGTTCTCATGTCTGTGTCATCCTCATGTTTATACACCTGCCTTTTCTCCA  
TCCTCGCCCATCGCTTTGGACACAATGTCTCTCGACCTTCCACATCATGTTGCCAATCTC  
TACATTGTTATCCCACCTGCACTCAACCCCATGGTTTACGGAGTGAAGACCAAGCAGATCA  
50 GAGATAAGGTTATACTTTTGTGTTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

**AOLFR148 sequences:**

MPTVNHSGTSHTVFHLGIPGLQDQHMWISIPFFISYVTALLGNSLLIFILTKRSLHEPMYLFLC  
MLAGADIVLSTCTIPQALAIWFWRAGDISLDRCTQLFFIHSTFISESGILLVMAFDHYIAICYPLR  
55 YTTILTNALIKKICVTVSLRSYGTIFPIIFLLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINIWYG

FSILMSTVVLDVVLIFISYMLILHAVFHMPSPDACHKALNTFGSHVCIILFYGSGIFTILTQRFRGR  
HIPPCIHIPLANVCILAPPMLNPIIYGIKTKQIQEQVVQFLFIKQKITLV (SEQ ID NO: 273)

5 ATGCCTACTGTAAACACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG  
GCCTACAGGACCAGCACATGTGGATTTCTATCCCATTCTTCATTTCTATGTCACCGCCCTT  
CTTGGGAACAGCCTGCTCATCTTCATTATCCTCACAAAGCGCAGCCTCCATGAACCCATGT  
ACCTCTTCTCTGTCATGCTGGCTGGAGCAGACATTGTCCTCTCCACGTGCACCATTCTCAG  
GCCTTAGCTATCTTCTGGTTCGGTCTGGGGACATCTCCCTGGATCGTTGCATCACTCAGCT  
10 CTTCTTCATCCATTCCACCTTCATCTCTGAGTCAGGGATCTTGCTGGTGATGGCCTTTGACC  
ACTATATTGCCATATGCTACCCACTGAGGTACACCACCATTCTTACAAATGCTCTGATCAA  
GAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTTCCCTATCATATTTCTTT  
TAAAAAGATTGACTTTCTGCCAGAATAATATTATCCACACACCTTTTGTGAACACATTGG  
CCTAGCCAAATATGCATGTAATGACATTGCAATAAACATTTGGTATGGGTTTTCATTCTA  
15 ATGTCGACGGTGGTCTTAGATGTTGTACTAATTTTATTTCTATATGCTGATTCTCCATGC  
TGCTTCCACATGCCTTCTCCAGATGCTTGCCACAAAGCTCTCAACACATTGGCTCCCATT  
TCTGCATCATCATCCTCTTTTATGGGTCTGGCATCTTCACAATCCTTACCCAGAGGTTTGG  
CGCCACATTCCACCTTGTATCCACATCCCCTTGGCTAATGTCTGCATTCTGGCTCCACCTAT  
GCTGAATCCCATTATTTATGGGATCAAACCAAGCAAATCCAGGAACAGGTGGTTCAGTTT  
20 TTGTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)

**AOLFR149 sequences:**

MSNASLLTAFILMGLPHAPALDAPLFGVFLVYVLTVLGNLLILLVIRVDSHLHTTMYYFLTNL  
SFIDMWFSVTVPKLLMTLVFPSGRAISFHSQMAQLYFFHFLGGTECFLYRVMSCDRYLAI  
25 LRYTSMMTGRSCTLLATSTWLSGSLHSAVQAILTFHLPYCGPNWQHYLDCDAPPILKLACADTS  
AIETVIFVTVGIVASGCFVLIVLSYVSIVCSILRIRTSEKHFRAFQTCASHCIVVLCFFGPGFLFIYLR  
PGSRKAVDGVVAVFYTVLTPLLNPVVYTLRNKEVKKALLKLKDKVAHSQSK (SEQ ID NO:  
275)

30 ATGTCCAACGCCAGCCTACTGACAGCGTTCATCCTCATGGGCCTTCCCCATGCCCCAGCGC  
TGGACGCCCCCTCTTTGGAGTCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT  
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTACTACTTCTCA  
CCAACCTGTCGTTTATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAATTGCTGATGAC  
TTTGGTGTTCCTAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCTATTTCT  
35 TTTACTTCTAGGGGGCACCAGTGTTCCTCTACAGGGTCATGTCCTGTGATCGCTACCT  
GGCCATCAGTTACCCGCTCAGGTACACCAGCATGATGACTGGGCGCTCGTGTACTCTTCTG  
GCCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGGCCATATTGACTTTCC  
ATTTGCCCTACTGTGGACCCAACTGGATCCAGCACTATTTGTGTGATGCACCGCCCATCCT  
GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCATTTTGTGACTGTTGGAATA  
40 GTGGCCTCGGGCTGCTTTGTCTGTAGTAGCTGTCTCTATGTGTCCATCGTCTGTTCCATCCT  
GCGGATCCGCACCTCAGAGGGGAAGCAGACGCTTTCAGACCTGTGCCTCCCAGTATC  
GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCACTTTACCTGAGGCCAGGCTCCAGGAAGC  
TGTGGATGGAGTTGTGGCCGTTTTCTACACTGTGCTGACGCCCCCTTCTCAACCCTGTTGTGT  
ACACCCTGAGGAACAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCAC  
45 ATTCTCAGAGCAAATAG (SEQ ID NO: 276)

**AOLFR150 sequences:**

MELGNVTRVKEFIFLGLTQSQDQSLVFLFLCLVYMTLLGNLLIMVTVTCESRLHTPMYFLLR  
NLAILDICFSSTTAPKVLLDLLSKKKTISYTSMTQIFLHLLGGADIFSLSVMAFDCYMAISKPL  
HYVTIMSRGQCTALISASWMGGFVHSIVQISLLPLPFCGPNVLDTFYCDVPQVLKLTCTDTFA  
50 LEFLMISNNGLVTTLWFIFLLVSYTVILMTLRSQAGGGRRKAISTCTSPHHCGRPFAFCALHCLC  
PALHCPPHRKGHLCHLHCHLPSAEPFDLHSEEPGNEVSHEKTEEKTRAF (SEQ ID NO: 277)

55 ATGGAGTTGGGAAATGTCACCAGAGTAAAGAATTTATATTTCTGGGACTTACTCAATCCC  
AAGACCAGAGTTTGGTCTTGTTCTTTTTTATGTCTTGTTGATGACGACTCTGCTGGGA  
AACCTCCTCATCATGGTCACCGTGACCTGTGAGTCTCGCCTTCACACCCCCATGTACTTCT  
GCTCCGCAATCTAGCCATCCTTGACATCTGCTTCTCCTCCACAACCTGCTCCTAAAGTCTTGC

TGGACCTTCTGTCAAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTTCT  
 CTTCCACCTCCTTGGTGGGGCAGACATTTTTTCTCTCTGTGATGGCGTTTGACTGCTACA  
 TGGCCATCTCCAAGCCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT  
 CATCTCTGCCTCTTGGATGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTTGCTGC  
 5 CTCTCCCTTTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCCTC  
 AAACCTCACTTGCACTGACACTTTTGCTCTTGAGTTCTTGATGATTTCCAACAATGGCCTGGT  
 CACTACCCTGTGGTTTATCTTCCTGCTTGTGTCTACACAGTCATCCTAATGACGCTGAGGT  
 CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTTGACCTCCCCACATCACTGTG  
 GTGACCCTGCATTTTGTGCCCTGCATCTATGTCTATGCCCCGCCCTTCACTGCCCTCCCCAC  
 10 AGAAAAGGCCATCTCTGTACCTTCACTGTATCTCCCTCTGCTGAACCCCTTGATCTACA  
 CTCTGAGGAACCAGGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT  
 CTGA (SEQ ID NO: 278)

**AOLFR151 sequences:**

15 MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLIRTNSHLQTPMYFFLGHLS  
 FVDICYSSNVTPNMLHNLSEKQKISYAGCFTQCLLFIALVITEFYILASMAIDRYVAICSPHY  
 SRMSKNICVCLVTIPYMYGFLSGFSQSLTFHLSFCGSLEINHFCADPPLIMLACSDTRVKMA  
 MFVVAGFNLSSSLFIILLSYLFIFAIFRIRSAEGRHKAFSTCASHLTIVTLFYGTLCMYVRPSE  
 KSVEESKITAVFYTFPLSPMLNPLIYSLRNTDVLAMQMQMIRGKSFHKIAV (SEQ ID NO: 279)

20 ATGTTCTCCCCAAACCACACCATAGTGACAGAATTCATTCTCTTGGGACTGACAGACGACC  
 CAGTGCTAGAGAAGATCCTGTTTGGGGTATTCCTTGCATCTACCTAATCACACTGGCAGG  
 CAACCTGTGCATGATCCTGCTGATCAGGACCAATCCCACCTGCAAACACCCATGTATTC  
 TTCCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTACTCCAAATATGCT  
 25 GCACAATTTCTCTCAGAACAGAACCATCTCCTACGCTGGATGCTTCACACAGTGTCTT  
 CTCTTCATCGCCCTGGTGATCACTGAGTTTTACATCCTTGCTTCAATGGCATTGGATCGCTA  
 TGTAGCCATTTGCAGCCCTTTGCATTACAGTTCCAGGATGTCCAAGAACATCTGTGTCTGT  
 CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTTCTCTCAGTCACTGCTAACCTT  
 TCACTTATCCTTCTGTGGCTCCCTTGAAATCAATCATTTCTACTGCGCTGATCCTCCTCTTA  
 30 TCATGCTGGCCTGCTCTGACACCCGTGTCAAAAAGATGGCAATGTTTGTAGTTGCAGGCTT  
 TAATCTCTCAAGCTCTCTCTTCATCATTCTTCTGTCCTATCTTTTCATTTTTGCAGCGATCTT  
 CAGGATCCGTTCTGCTGAAGGCAGGCACAAAGCCTTTTCTACGTGTGCTTCCCACCTGACA  
 ATAGTCACTTTGTTTTATGGAACCCCTCTCTGCATGTACGTAAGGCCTCCATCAGAGAAGT  
 CTGTAGAGGAGTCCAAAATAACTGCAGTCTTTATACTTTTTTGAGCCCAATGCTGAACCC  
 35 ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA  
 AAATCCTTTTATAAAATTGCAGTTTAG (SEQ ID NO: 280)

**AOLFR152 sequences:**

MDQINHTNVKEFFLELTRSRELEFFLVVFFAVYVATVLGNALIVVTITCESRLHTPMYFLLRN  
 40 KSVLDIVFSSITVPKFLVØLLSDRKITISYNDICMAQIFFHFAGGADIFFLSVMAYDRYLAIKPL  
 HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPFPFCGPNTLDAFYCYVLQVVKLACTDT  
 FALELFMISNGLVTLLWFLLLGSYTVILVMLRSHSGEGRNKALSTCTSHMLVVTLHFVPCV  
 YIYCRPFMTLPMDTTISINNTVITPMLNPIIYSLRNQEMKSAMQRLQRRLLGPSESRRKWG (SEQ ID  
 NO: 281)

45 ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTTCCCTGGAACCTTACACGTTCCC  
 GAGAGCTGGAGTTTTTCTTGTTGTGGTCTTCTTGCTGTGTATGTAGCAACAGTCCTGGG  
 AAATGCACTCATTGTGGTCACTATTACCTGTGAGTCCCGCCTACACACTCCTATGTACTTTC  
 TCCTGCGGAACAAATCAGTCCTGGACATCGTTTTTTCATCTATCACCGTCCCCAAGTTCCTG  
 50 GTGGATCTTTTATCAGACAGGAAAACCATCTCCTACAATGACTGCATGGCACAGATCTTTT  
 TCTTCCACTTTGCTGGTGGGGCAGATATTTTTTCTCTCTGTGATGGCCTATGACAGATAC  
 CTGCAATCGCCAAGCCCCTGCACTATGTGACCATGATGAGGAAAGAGGTGTGGGTGGCC  
 TTGGTGGTGGCTTCTTGGGTGAGTGGTGGTTTGCATTCAATCATCCAGGTAATTCTGATGC  
 TTCCATTCCCCTTCTGTGGCCCCAACACACTGGATGCCTTCTACTGTTATGTGCTCCAGGTG  
 55 GTAAAACTGGCCTGCACTGACACCTTTGCTTTGGAGCTTTTCATGATCTCTAACAACGGAC  
 TGGTGACCTGCTCTGGTTCTCTGCTCCTGGGCTCCTACACTGTCATTCTGGTGATGCTG

AGATCCCACTCTGGGGAGGGGCGGAACAAGGCCCTCTCCACGTGCACGTCCCACATGCTG  
GTGGTGACTCTTCACTTCGTGCCTTGTGTTTACATCTACTGCCGGCCCTTCATGACGCTGCC  
CATGGACACAACCATATCCATTAATAACACGGTCAATTACCCCCATGCTGAACCCCCATCATC  
TATTCCCTGAGAAATCAAGAGATGAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG  
5 CCTCCGAGAGCAGAAAATGGGGGTGA (SEQ ID NO: 282)

**AOLFR153 sequences:**

MSKTSLVTAFLTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNL  
FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAI  
10 RYTSMMMSGSRCALLATSTWLSGLHSAVQTLTFHLPYCGPNQIQHYLCDAPPILKLACADTSA  
NEMVIFVDIGLVASGCFLIVLSYVSIVCSILRIHTSEGRHRAFQTCASHCIVVLCFFVXCVFIYLR  
PGSRDVVDGVVAIFYTVLTPLLNPVYTLRNKEVKKAVLKLKRDKVAHSQGE (SEQ ID NO:  
283)

15 ATGTCCAAGACCAGCCTCGTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC  
TGGACGCCCCACTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT  
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCCTCA  
CCAACCTGTCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCAAAATGCTGATGAC  
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT  
20 TCCACTTCTGGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCCTATGATCGCTACTTG  
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGATGTGCCCTCCTGG  
CCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT  
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTATTTGTGTGATGCACCGCCCATCTGA  
AACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGGACATTGGGCTAGT  
25 GGCCTCGGGCTGCTTTCTCCTGATAGTGTCTTATGTGTCCATCGTCTGTTCCATCCTGC  
GGATCCACACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGCATCGT  
GGTCTTTTGCTTTTTTGTNNCTGTGTTTTTCACTTACCTGAGACCAGGCTCCAGGGACGTCG  
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACACCCCTTCTCAACCCTGTTGTGTAC  
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT  
30 TCTCAGGGAGAATAA (SEQ ID NO: 284)

**AOLFR156 sequences:**

MCWAMPSPFTGSSTRNMESRNQSTVTEFIFTGFPQLQDGSLLYFFPLLFIYTFIIDNLLIFSAVRL  
DTHLGNPMYNFISIFSLEIWTATIPKMLSNLISEKKAISMTGCILQMYFFHSLNSEGILLTT  
35 MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGFLILLPEIVMISTLPFCGPNQIHQIFCDLVP  
VLSLACTDTSMLIEDVIHAVTHITFLIALSYVRIVTVILRIPSSEGRQKAXSTCAGHLMVFLIFFG  
SVSLMYLRFSNTYPPVLDTAIALMFTVLAPFFNPIIYSLRNKDMNNAIKKLFCLQKVLNKP  
GG (SEQ ID NO: 285)

40 ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA  
ACCAATCAACAGTGACTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT  
CCTGTACTTCTTTCTTTACTTTTCATCTATACTTTTATTATCATTGATAACTTATTAATCTT  
CTCTGCTGTAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT  
CCTTTCTGGAGATCTGGTACACCACAGCCACCATTCCTCAAGATGCTCTCCAACCTCATCAG  
45 TGAAAAGAAGGCCATCTCAATGACTGGCTGCATCTTGACAGATGTATTTCTTCCACTCACTT  
GAAAACTCAGAGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA  
ACCCTCTTCGCTATCAAATGATCATGACCCCCCGGCTCTGTGCTCACCTCTCTGCAGGTTCC  
TGCCTCTTCGGTTTCCTTATCCTGCTTCCCGAGATTGTGATGATTTCCACACTGCCTTTCTG  
TGGGCCCCAACCAATCCATCAGATCTTCTGTGACTTGGTCCCTGTGCTAAGCCTGGCCTGT  
50 ACAGACACGTCCATGATTCTGATTGAGGATGTGATTGCTGTGACCATCATCATTACCT  
TCCTAATCATTGCCCTGTCTATGTAAGAATTGTCACTGTGATATTGAGGATTCCTCTTCT  
GAAGGGAGGCAAAAGGCTNTTCTACCTGTGCAGGCCACCTCATGGTCTTCTGATATTCT  
TTGGCAGTGTATCACTCATGTAATTGCGTTTCAGCAACACTTATCCACCAAGTTTGGACAC  
AGCCATTGCACTGATGTTTACTGTACTTGCTCCATTCTTCAATCCCATCATTTATAGCCTGA  
55 GAAACAAGGACATGAACAATGAATTAATAAACTGTTCTGTCTTCAAAAAGTGTTGAACA  
AGCCTGGAGGTAA (SEQ ID NO: 286)

**AOLFR157 sequences:**

5 MAMDNVTAVFQFLIGISNYPQWRDTFFTLVLIYLSLTLGNGFMIFLIHFDPNLHTPIYFFLSNL  
SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAISNP  
LRYSVVMNGPVCVCLVATSWGTSLVLTAMLILSLRLHFCGANVINHFACILSLIKLTCSDTSL  
NEFMILITSIFTL LLPFGFVLLSYIRIAMAIIRSLQGR LKAFTTCGSHLT VVTIFYGSAISMYMKT  
QSKSSPDQDKFISVFY GALT PMLNPLIYSLRKKDVKRAIRKVMLKRT (SEQ ID NO: 287)

10 ATGGCCATGGACAATGTCACAGCAGTGTTCAGTTTCTCCTTATTGGCATTCTAACTATCC  
TCAATGGAGAGACACGTTTTTACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG  
AATGGATTATGATCTTTCTTATTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT  
CCTTAGTAACCTGTCTTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG  
TGCATTGTTTCTCTACCCATCCCTACCTCTCTTATCCCCGATGTTTGGCTCAAACGAGTGTC  
TCCTTGGCTTTGGCCACAGCAGAGTGCTCCTACTGGCTGCCATGGCCTATGACCGTGTGG  
15 TTGCTATCAGCAATCCCCTGCGTTATTCACTGGTGTATGAATGGCCCAGTGTGTGTCTGCTT  
GGTTGCTACCTCATGGGGGACATCACTTGTGCTCACTGCCATGCTCATCCTATCCCTGAGG  
CTTCACTTCTGTGGGGCTAATGTCATCAACCAATTTGCCTGTGAGATTCTCTCCCTCATTA  
GCTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCATCACCAAGTATCTTACCC  
TGCTGCTACCATTTGGGTTGTTCTCCTCTCTACATACGAATTGCTATGGCTATCATAAGG  
20 ATTCGCTCACTCCAGGCGAGGCTCAAGGCCTTTACCACATGTGGCTCTCACCTGACCGTGG  
TGACAATCTTCTATGGGTGAGCCATCTCCATGTATATGAAAACCTCAGTCCAAGTCTCCCC  
TGACACAGGACAAGTTTATCTCAGTGTTTTATGGAGCTTTGACACCCATGTTGAACCCCTG  
ATATATAGCCTGAGAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAAGG  
ACATGA (SEQ ID NO: 288)

25

**AOLFR158 sequences:**

30 MKAGNFSDTPEFFLLGLSGDPELQPIFLFMSMYLATMLGNLLILAVNSDSHLHTPMYFLLSI  
LSLVDICFTSTTMPKMLVNIQAQASINYTGCLTQICFVLVFGLENGILVMMAYDRFVAICHP  
LRYNVIMNPKLCGLLLLLSFIVSVLDALLHTLMVLQLTFCIDLEIPHFFCELAHILKLACSDVLIN  
NILVYLVTSLGVPVLSGIIFS YTRIVSSVMKIPSAGGKYKAFSICGSHLIVVSLFYGTGFGVYLSS  
GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKDMLKALRK LISRIPSFH (SEQ ID NO: 289)

35 ATGAAAGCAGGAAACTTCTCAGACACTCCAGAATTCTTCTCTTGGGATTGTGAGGGGATC  
CGGAGCTGCAGCCCATCCTCTTCATGCTGTTCTGTCCATGTACCTGGCCACAATGCTGGG  
GAACCTGCTCATCATCCTGGCCGTCAACTCTGACTCCCACCTCCACACCCCCATGTA CTTC  
TCCTCTCTATCCTGTCTTGGTTCGACATCTGTTTACCTCCACCACGATGCCCAAGATGCTG  
GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTACCCAAATCTGCT  
TTGTCTGGTTTTTTGTTGGATTGGAAAATGGAATTCTGGTCATGATGGCCTATGATCGATT  
TGTTGGCCATCTGTCACCCACTGAGGTACAATGTCATCATGAACCCCAA CTCTGTGGGCTG  
40 CTGCTTCTGCTGTCTTCATCGTTAGTGTCCTGGATGCTCTGCTGCACACGTTGATGGTGCT  
ACAGCTGACCTTCTGCATAGACCTGGAAATTCCCCACTTTTCTGTGAACTAGCTCATATTC  
TCAAGCTCGCTGTTCTGATGTCCTCATCAATAACATCCTGGTGTATTTGGTGACCAGCCT  
GTAGGTGTTGTTCTCTCTCTGGGATCATTTTCTCTTACACACGAATTGTCTCTCTGTCA  
TGAAAATTCCATCAGCTGGTGGAAAGTATAAAGCTTTTCCATCTGCGGGTCACATTTAAT  
45 CGTTGTTTCTTGTGTTTATGGAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGCTACCCACT  
CCTCCAGGAAGGGTGCAATAGCATCAGTGATGTATACCGTGGTCACCCCATGCTGAACCC  
ACTCATTTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAACTAATATCTAG  
GATACCATCTTCCATTGA (SEQ ID NO: 290)

50 **AOLFR159 sequences:**

MGPRNQTA VSEFLMKVTEDPELKLIPFSLFMSMYLVITLGNLLILLAVISDSHLHTPMYFLLFN  
LSFTDICLTTTTVPKILVNIQAQNSITYTGCLTQICLVLVFAGLESCFLAVMAYDRYVAICHPL  
RYTVLMNVHFWGLLILSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCEVVQVIKLACSDTL  
INNILYFASSVFGAIPLSGIIFSYSQIVTSVLRMP SARGKYKAFSTCGCHLSVFSLFYGTAFGVYIS  
55 SAVAESSRITAVASVMYTVVPMNPFYSLRNKEMKKALRK LIGRLFPF (SEQ ID NO: 291)



ATGGGACCCAGAAACCAAACAGCTGTTTCAGAATTTCTTCTCATGAAAGTGACAGAGGAC  
 CCAGAACTGAAGTTAATCCCTTTTACAGCCTGTTCTGTCCATGTACCTGGTCACCATCCTGG  
 GGAACCTGCTCATTCTCCTGGCTGTCATCTCTGACTCCCACCTCCACACCCCCATGTACTTC  
 CTTCTCTTTAATCTCTCCTTTACTGACATCTGTTTAAACCACAACCACAGTCCCAAAGATCCT  
 5 AGTGAACATCCAAGCTCAGAATCAGAGTATCACTTACACAGGCTGCCTCACCCAGATCTGT  
 CTTGTCTTGGTTTTTGCTGGCTTGAAAGTTGCTTTCTTGCAGTCATGGCCTACGACCGCTA  
 TGTGGCCATTTGCCACCCACTGAGGTACACAGTCTCATGAATGTCCATTTCTGGGGCTTG  
 CTGATTCTTCTCTCCATGTTTCATGAGCACTATGGATGCCCTGGTTCAGAGTCTGATGGTATT  
 GCAGCTGTCCCTCTGCAAAAACGTTGAAATCCCTTTGTTCTTCTGTGAAGTCGTTTCAGGTC  
 10 ATCAAGCTCGCCTGTTCTGACACCCTCATCAACAACATCCTCATATATTTTGCAAGTAGTGT  
 ATTTGGTGCAATTCCTCTCTCTGGAATAATTTTCTCTTATTCTCAAATAGTCACCTCTGTTC  
 TGAGAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTCCACCTGTGGCTGTACCTCTC  
 TGTTTTTCTCTTGTCTATGGGACAGCTTTTGGGGTGTACATTAGTTCTGCTGTTGCTGAGT  
 CTTCCCGAATTACTGCTGTGGCTTCAGTGATGTACACTGTGGTCCCTCAAATGATGAACCC  
 15 CTTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAAACTTATTGGTAG  
 GCTGTTTCTTTTAG (SEQ ID NO: 292)

**AOLFR160 sequences:**

20 MPMQLLLTDFIIFSIRFIINSMEARNQTAISKFLLGLIEDPELQPVLFSLFSLMYLVLTILGNLLILL  
 AVISDSHLHTPMYFFLSNLSFLDICLSTTTIPKMLVNIQAQNRSTYSGLTQICFVLFFAGLENC  
 LLAAMAYDRYVAICHPLRYTVIMNPRLCGLLILLSLTSVNNALLLSLMVLRSLFCTDLEIPLFF  
 CELAQVIQLTCSDTLNNILYFAACIFGGVPLSGIILSYTQITSCVLRMPASGKHKAIVSTCGSHL  
 SIVLLFYGAGLGVYISSVVTDSPRKTAVASVMYSVFPQMVNPFYISLRNKDMKGLRKFGRIP  
 SLLWCAICFGFRFLE (SEQ ID NO: 293)

25 ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTTCCATCAGATTCATCATCAACAG  
 CATGGAAGCGAGAAACCAAACAGCTATTTCAAATTCCTTCTCCTGGGACTGATAGAGGAT  
 CCGGAACTGCAGCCCGTCTTTTACGCCTGTTCTGTCCATGTACTGGTCAACCATCCTGGG  
 GAACCTGCTCATCCTCTTGGCTGTCATCTCTGACTCTCACCTCCACACCCCCATGTACTTCT  
 30 TCCTCTCCAATCTCTCCTTTTGGACATTTGTTTAAAGCACAACCACGATCCCAAAGATGCTG  
 GTGAACATCCAAGCTCAGAATCGGAGCATCACGTACTCAGGCTGCCTCACCCAGATCTGCT  
 TTGTCTTGTTTTTTGCTGGCTTGAAAAATTGTCTCCTTGCAAGTGGCCTATGACCGCTAT  
 GTGGCCATTTGTACCCCCCTTAGATACACAGTCATCATGAACCCCGCCTCTGTGGCCTGC  
 TGATTCTTCTCTCTCTGTTGACTAGTGTGTGAATGCCCTTCTTCTCAGCCTGATGGTGTG  
 35 AGGCTGTCTCTGTCACAGACCTGGAATCCCGCTCTTCTTCTGTGAAGTGGCTCAGGTCA  
 TCCCACTCACCTGTTTCAGACACCTCATCAATAACATCCTGATATATTTTGAGCTTGCATA  
 TTTGGTGGTGTCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACCTCCTGTGTTTT  
 GAGAATGCCATCAGCAAGTGGAAGCACAAGCAGTTTCCACCTGTGGGTCTCACCTCTCC  
 ATTGTTCTCTTGTCTATGGGGCAGGTTTGGGGGTGTACATTAGTTCTGTGGTACTGACTC  
 40 ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTGTTCCCTCAAATGGTGAACCCC  
 TTTATCTATAGTCTGAGGAATAAGGACATGAAAGGAACCTTGAGGAAGTTCATAGGGAGG  
 ATACCTTCTCTTCTGTGGTGTGCCATTTGCTTTGGATTTCAGGTTTCTAGAGTAA (SEQ ID  
 NO: 294)

**AOLFR161 sequences:**

45 MEPRNQTSASQFILLGLSEKPEQETLLFSLFFCMYLVMMVGNLLIILAIIDSIDLHTPMYFFLANL  
 SLVDFCLATNTIPKMLVSLQTGSKAISYPCCLIQMYFFHFFGIVDSVIAMMAYDRFVAICHPLH  
 YAKIMSLRLCRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR  
 IFILIVAGMVIATPFVCILASYARILVAIMKVPSAGGRKKAFSTCSSHLSVVALFYGTTIGVYLCF  
 50 SSVLTTVKEKASAVMYTAVTPMLNPFYISLRNRDLKGALRKLVRNKITSSS (SEQ ID NO: 295)

55 ATGGAACCAAGAAACCAAACAGTGCATCTCAATTCATCCTCCTGGGACTCTCAGAAAAGC  
 CAGAGCAGGAGACGCTTCTCTTTTCCCTGTTCTTCTGCATGTACCTGGTCATGGTCGTGGG  
 GAACCTGCTCATCATCCTGGCCATCAGCATAGACTCCCACCTCCACACCCCCATGTACTTCT  
 TCCTGGCCAACCTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCCTAAGATGCT  
 GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCCTGATCCAGATGTAC

TTCTTCCATTTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGTT  
 CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTGCGCTG  
 CTGGTCGGCGCCCTCTGGGCGTTTTCTGCTTCATCTCACTCACTCACATCCTCCTGATGGC  
 CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC  
 5 TCCGACTTTCGTGCACGGACACCTCTGTGAATAGGATCTTCATCCTCATTGTGGCAGGGAT  
 GGTGATAGCCACGCCCTTTGTCTGCATCCTGGCCTCCTATGCTCGCATCCTTGTGGCCATCA  
 TGAAGGTCCCCTCTGCAGGCGGCAGGAAGAAAGCCTTCTCCACCTGCAGCTCCACCTGTC  
 TGTGGTTGCTCTCTTCTATGGGACCACCATTTGGCGTCTATCTGTGTCCCTCCTCGGTCCTCA  
 10 CTTGTTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCACCCCCATGCTGAATCC  
 CTTTCATCTACAGCTTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG  
 AAAGATCACCTCATCTTCCTGA (SEQ ID NO: 296)

#### AOLFR162 sequences:

15 MMRLMKEVRGRNQTEVTEFLLLGLSDNPDLQGVLFALFLLIYMANMVGNLGMIVLIKIDLCLH  
 TPMYFFLSSLFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFFGSFLGTECFLLAMMA  
 YDRYAAIWNPLLYPVLVSGRICFLLIATSFAGCGNAIHTGMTFRLSFCGSNRINHFYCDTPPL  
 LKLSCTDTHFNGIVIMAFSSFIVISCVMIIVLISYLCIFIAVLKMPISLEGRHKAFSTCASYLMAVTIF  
 FGTILFMYLRPTSSYSMEQDKVVSFYTIVIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID  
 NO: 297)

20 ATGATGAGACTTATGAAAGAGGTTTCGAGGCAGAAATCAAACAGAAGTAACAGAATTTCTC  
 CTCTTAGGACTTTCCGACAATCCAGATCTACAAGGAGTCCTCTTTGCATTGTTTCTGTTGAT  
 CTATATGGCAAACATGGTGGGCAATTTGGGGATGATTGTATTGATTAAAGATTGATCTCTGT  
 CTCCACACCCCCATGTATTCTTTCTCAGTAGCCTCTCTTTTGTAGATGCCTCTTACTCTTCT  
 25 TCCGTCACCTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCATG  
 GATGTGCTGCCCAGTTCTACTTCTTTGGCTCCTTCCTGGGGACTGAGTGCTTCCTGTTGGCC  
 ATGATGGCATATGACCGCTATGCAGCCATTTGGAACCCCTGCTCTACCCAGTTCTCGTGT  
 CTGGGAGAATTTGCTTTTTGCTAATAGCTACCTCCTTCTTAGCAGGTTGTGGAAATGCAGC  
 CATAACACAGGGATGACTTTTAGGTTGTCTTTTGTGGTTCTAATAGGATCAACCATTCT  
 30 ACTGTGACACCCCGCCACTGCTCAAACCTCTCTTGTCTGATACCCACTTCAATGGCATTGTG  
 ATCATGGCATTCTCAAGTTTTATTGTCATCAGCTGTGTTATGATTGTCCTCATTTCCTACCT  
 GTGTATCTTCATTGCCGCTTGAAGATGCCTTCGTTAGAGGGGCAGGCACAAAGCCTTCTCC  
 ACCTGTGCCTCTTACCTCATGGCTGTCACCATATTCTTTGGAACAATCCTCTTCATGTACTT  
 GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTTGTCTCTGTCTTTTATACAGTA  
 35 ATAATCCCTGTGCTAAATCCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCC  
 TAAAGAAGATCTTATGGAAACACATCTTGTAG (SEQ ID NO: 298)

#### AOLFR163 sequences:

40 MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVYSLTVVGNSTLIVLICNDSCLHTPMYFFTGN  
 LSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL  
 LYAQAMSIKLCALLVAVSYCGGFINSIIKKTFSFNFCRENIIDFFCDLLPLVELACGEKGGYK  
 IMMYFLLASNVICPAVLILASYLFIITSVLRISSSKGYLKAFTSCSSHLTSVTLYYGSILYIYALPRS  
 SYSFDMDKIVSTFYTVVFPMLNLMISLRNKDVKEALKKLLP (SEQ ID NO: 299)

45 ATGCAGAGGAGCAATCATACAGTGACTGAGTTTATACTGCTGGGCTTCACCACAGACCCA  
 GGAATGCAGCTGGGCTCTTCGTGGTGTTCCTGGGCGTGTACTCTCTCACTGTGGTAGGAA  
 ATAGCACCTCATCGTGTGATCTGTAATGACTCCTGCCTCCACACACCCATGTATTTTTTC  
 ACTGGAATCTGTGCTTTCTGGATCTCTGGTATTCTTCTGTCTACACCCCAAAGATCCTAGT  
 50 GACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCAGTTCTTCTCT  
 CTGCAGGCTTGGCCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT  
 GGCCATCTCCAAGCCCCTGCTTTATGCCAGGCCATGTCCATAAAGCTGTGTGCATTGCTG  
 GTAGCAGTCTCATATTGTGGTGGCTTTATTAACCTCTTCAATCATCACCAGAAAACGTTTTTC  
 CTTTAACTTCTGCCGTGAAAACATCATTGATGACTTTTTCTGTGATTGTGCTTCCCTTGGTGG  
 AGCTGGCCTGTGGCGAGAAGGGCGGCTATAAAATTATGATGTACTTCTGCTGGCCTCCAA  
 55 TGTTCATCTGCCCCGAGTGCTCATCCTGGCCTCCTACCTCTTTATCATCACCAGTGTCTTGA  
 GGATCTCCTCCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCCTCCACCTGACCTCT

GTCACCTTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCCAGATCTAGCTATTCTTT  
TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATTCCCCATGTTGAATCTCATG  
ATCTACAGCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAACTTCTCCCATAA (SEQ  
ID NO: 300)

5

**AOLFR164 sequences:**

MFLTERNTTSEATFTLLGFS DYLELQIPLFFVFLAVYGFSVVGNLGMIVIIKINPKLHTPMYFFLN  
HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFFCTFVVTTELILFAVMA YDHFVAICNP  
LLYTV AISQKLCAMLVVVLYAWGVACSLTLACSALKLSFHGFNTINHHFCELSLISLSYPDSYL  
10 SQLLLFTVATFNEISTLLIILTSYAFIIVTT LKMPSASGHRKVFSTCASHLTAITIFHG TILFLYCV P  
NSKNRHTVKVASVFYTVVIPLLNPLIYSLRNKDVKDAIRKIINTKYFHIKHRHWYPFNFVIEQ  
(SEQ ID NO: 301)

ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACCTCTCTTGGGCTTCTCAG  
15 ATTACCTGGAAGTCAAATTTCCCTCTTCTTTGTATTTCTGGCAGTCTACGGCTTCAGTGTG  
GTAGGGAATCTTGGGATGATAGTGATCATCAAAATTAACCCAAAATTGCATACCCCCATGT  
ATTTTTTCTCAACCACCTCTCCTTTGTGGATTTCTGCTATTCTCCCATCATTGCTCCCATGA  
TGCTGGTGAACCTGGTTGTAGAAGATAGAACCATTTCATTCTCAGGATGTTTGGTGCAATT  
CTTTTTCTTTTGACCTTTGTAGTGACTGAATTAATTCTATTTGCGGTGATGGCCTATGACC  
20 ACTTTGTGGCCATTTGCAATCCTCTGCTCTACACAGTTGCCATCTCCCAGAAACTCTGTGCC  
ATGCTGGTGGTTGTATTGTATGCATGGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG  
CTTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTCTTCTGTGAGTTATCCTCC  
CTGATATCACTCTCTTACCCTGACTCTTATCTCAGCCAGTTGCTTCTTTTCACTGTTGCCAC  
TTTAATGAGATAAGCACACTACTCATCATTCTGACATCTTATGCATTTCATCATTGTACCA  
25 CCTTGAAGATGCCTTCAGCCAGTGGGCACCGCAAAGTCTTCTCCACCTGTGCCTCCACCT  
GACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTCTACTGTGTACCCAACTCCAAAA  
ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCCTGTTGAA  
TCCCCTGATCTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT  
ACAAAATATTTTCATATTAACATAGGCATTGGTATCCATTTAATTTGTTATTGAACAATA  
30 A (SEQ ID NO: 302)

**AOLFR165 sequences:**

MAVGRNNTIVTKFILLGLSDHPQMKIFLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL  
SNLSFLDICVVSSTAPKMLS DIITEQKTISFVGCATQYFVFCGMGLTECFLLAAMAYDRYAAICN  
35 PLYTVLISHTLCLKMVVGAYVGGFLSSFIETYSVYQHDFCGPYMINHFFCDLPPVLALSCSDTF  
TSEVVT FIVSVVVGIVSVLVVLISYGYIVA AVVKISSATGRTKAFSTCASHLTA VTLFYGSGFFM  
YMRPSSSYSLNRDKVVSIFYALVIPVNP IISFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG  
(SEQ ID NO: 303)

ATGGCTGTAGGAAGGAACAACAATTGTGACAAAATTCATTCTCCTGGGACTTTCAGACC  
40 ATCCTCAAATGAAGATTTTCTTTTCATGTTATTTCTGGGGCTCTACCTCCTGACGTTGGCC  
TGGAACCTTAAGCCTCATTGCCCTCATTAAGATGGACTCTCACCTGCACATGCCCATGTACT  
TCTTCTCAGTAACCTGTCCTTCTGGACATCTGCTATGTGTCCTCCACCGCCCCCTAAGATG  
CTGTCTGACATCATCACAGAGCAGAAAACCATTTCCTTTGTTGGCTGTGCCACTCAGTACT  
45 TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTTCTCCTGGCAGCTATGGCCTATGACCG  
GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCCTCATATCCCATACACTTTGTTAA  
AGATGGTGGTTGGCGCCTATGTGGGTGGATTCTTAGTTCTTTCATTGAAACATACTCTGT  
CTATCAGCATGATTTCTGTGGGCCCTATATGATCAACCACTTTTCTGTGACCTCCCTCCAG  
TCCTGGCTCTGTCTGCTCTGATACCTTCACCAGCGAGGTGGTGACCTTCATAGTCAGTGTT  
50 TCGTGTGGAATAGTGTCTGTGCTAGTGGTCTCTGCTATCTTATGGTTACATTGTTGCTGCTGT  
TGTGAAGATCAGCTCAGCTACAGGTAGGACAAAGGCCTTCAGCACTTGTGCCTCTCACCTG  
ACTGCTGTGACCTCTTCTATGGTTCTGGATTCTTCATGTACATGCGACCCAGTTCAGCTA  
CTCCCTAAACAGGGACAAGGTGGTGTCCATATTCTATGCCTTGGTGATCCCCGTGGTGAAT  
CCCATCATCTACAGTTTTAGGAATAAGGAGATTAAAAATGCCATGAGGAAAGCCATGGAA  
55 AGGGACCCCGGATTTCTCACGGTGGACCATTCAATTTTATGACCTTGGGCTAA (SEQ ID  
NO: 304)

**AOLFR166 sequences:**

MEMENCTRVKEFIFLGLTQNREVSIVLFLFLLLVYVTTLLGNLLIMVTVTCE SRLHTPMYFLLH  
NLSIADICFSSITVPKVLVDLLSERKTISFNHCFTQMFLFHLIGGVDVFSLSVMALDRYVAISKPL  
5 HYATIMSRDHCIGLTVAAWLGGFVHSIVQISLLPLPFCGPNVLDTFYCDVHRVLKLAHTDIFIL  
ELLMISNNGLLTTLWFFLLLVSYIVILSLPKSQAGEGRRKAISTCTSHITVVTLHFVPCIYVYARP  
FTALPMDKAISVTFTVISPLLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

10 ATGGAGATGGAAAACCTGCACCAGGGTAAAAGAATTTATTTTCCTTGGCCTGACCCAGAATC  
GGGAAGTGAGCTTAGTCTTATTTCTTTTCTACTCTTGGTGTATGTGACAACTTTGCTGGGA  
AACCTCCTCATCATGGTCACTGTTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTTT  
GCTCCATAATTTATCTATTGCCGATATCTGCTTCTCTCCATCACAGTGCCCAAGGTTCTGG  
TGGACCTTCTGTCTGAAAGAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA  
15 TTCCACCTTATTGGAGGGGTGGATGTATTTTCTCTTTCGGTGTATGGCATTGGATCGATATG  
TGGCCATCTCCAAGCCCCTGCACTATGCGACTATCATGAGTAGAGACCATTGCATTGGGCT  
CACAGTGGCTGCCTGGTTGGGGGGCTTTGTCCACTCCATCGTGCAGATTTCCCTGTTGCTC  
CCACTCCCTTTCTGCGGACCCAATGTTCTTGACACTTTCTACTGTGATGTCCACCGGGTCT  
CAAACCTGGCCCATACAGACATTTTCATACCTTGAACCTACTAATGATTCCAACAATGGACTG  
CTCACCACTGTGGTTTTTCTGCTCTGTTGTCTTACATAGTCATATTATCATTACCCAA  
20 GTCTCAGGCAGGAGAGGAGGAGGAAAGCCATCTCCACCTGCACCTCCCACATCACTGT  
GGTGACCTGCATTTCTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCA  
TGGATAAGGCCATCTCTGTACCTTCACTGTCTATCTCCCTCTGCTCAACCCCTTGATCTAC  
ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCCT  
TCTGATAGAAAATAG \*SEQ ID NO: 306)

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**AOLFR167 sequences:**

MSITKAWNSSSVTMFILLGFTDHPQLALLFVTFGLGIYLTTLAWNLAFLIRGDTHLHTPMYFF  
LSNLSFIDICYSSAVAPNMLTDFWEQKTISFVGCAAQFFFFVGMGLSECLLLTAMAYDRYAAI  
SSPLLYPTIMTQGLCTRMVVGAYVGGFLSSLIQASSIFRLHFCGPNINHHFFCDLPPVLALSCSDT  
30 FLSQVVNFLVVVTVGGTSFLQLLISYGYIVSAVLKIPSAEGRWKACNTCASHLMVVTLFGTAL  
FVYLRPSSSYLLGRDKVVSFVSLVIPMLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID  
NO: 307)

35 ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCCTCCTGGGATTCA  
CAGACCATCCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCCTGGGCATCTATCTTACCACC  
CTGGCCTGGAACCTGGCCCTCATTTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA  
TGTACTTCTTCTAAGCAACTTATCTTTCACTGACATCTGCTACTCTTCTGCTGTGGCTCCC  
AATATGCTCACTGACTTCTTCTGGGAGCAGAAGACCATATCATTTGTGGGCTGTGCTGCTC  
AGTTTTTTTTCTTTGTGCGGCATGGGTCTGTCTGAGTGCCTCCTCCTGACTGCTATGGCATA  
40 GACCGATATGCAGCCATCTCCAGCCCCCTTCTTACCCCACTATCATGACCCAGGGCCTCT  
GTACACGCATGGTGGTTGGGGCATATGTTGGTGGCTTCCTGAGCTCCCTGATCCAGGCCAG  
CTCCATATTTAGGCTTCACTTTTGCAGACCCAACATCATCAACCACTTCTTCTGCGACCTCC  
CACCAGTCCTGGCTCTGTCTTGCTCTGACACCTTCCTCAGTCAAGTGGTGAATTTCTCGTG  
GTGGTCACTGTGCGGAGGAACATCGTTTCTTCAACTCCTTATCTCCTATGGTTACATAGTGT  
45 CTGCGGTCCTGAAGATCCCTTCAGCAGAGGGCCGATGGAAAGCCTGCAACACGTGTGCCT  
CGCATCTGATGGTGGTGACTCTGCTGTTTGGGACAGCCCTTTTCGTGTACTTGGCAGCCAG  
CTCCAGCTACTTGCTAGGCAGGGACAAAGGTGGTGTCTGTTTTCTATTGATTGGTGATCCCC  
ATGCTGAACCCTCTCATTTACAGTTTGAAGAACAAAGAGATCAAGGATGCCCTGTGGAAG  
GTGTTGGAAGGAAGAAAGTGTTTTCTTAG (SEQ ID NO: 308)

50

**AOLFR168 sequences:**

MEKINNVTETIFWGLSQSPEIEKVCFVVSFFYIIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV  
DICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMA YDRYVAICKPLHYM  
TIMNRETCKMMLLGTWVGFLHSIIQVALVVQLPFCGPNIDHYFCDVHPVLKLACTETIYIVG  
55 VVVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVIFFGPCTFMYMRPD

TTFSEDKMVAVFYTHITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO: 309)

5 ATGGAAAAAATAAACACGTAACCTGAATTCATTTTCTGGGGTCTTTCTCAGAGCCCAGAGA  
TTGAGAAAGTTTGTGGTGTCTTTCTTCTTCTACATAATCATTCTTCTGGGAAATCTC  
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTTAAGTCACCCATGTATTTCTTTCTCAG  
CTTCTTGTCTTTTGTGGACATTTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC  
TGTTAGCAAAGGACAAAACCATCTCCT1ATGTGGGGTGCATGTTGCAACTGCTTGGAGTAC  
ATTTCTTTGGTTGCACTGAGATCTTCATCCTTACTGTAATGGCCTATGATCGTTATGTGGCT  
10 ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT  
TAGGGACGTGGGTAGGTGGGTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAACCT  
ACCCTTTTGTGGACCCAATGAGATAGATCACTACTTTTGTGATGTTACCCTGTGTTGAAA  
CTTGCTGCACAGAAACATACATTGTTGGTGTGTTGTGACAGCCAACAGTGGTACCATTG  
CTCTGGGGAGTTTGTATCTTGCTAATCTCCTACAGCATCATCCTAGTTTCCCTGAGAAAG  
15 CAGTCAGCAGAAAGGCAAGCGCAAAGCCCTCTCCACCTGTGGCTCCACATTGCCATGGTCG  
TTATCTTTTTCGGCCCCCTGTACTTTTATGTACATGCGCCCTGATACGACCTTTTCAGAGGAT  
AAGATGGTGGCTGTATTTACACCATTATCACTCCCATGTTAAATCCTCTGATTTATACACT  
GAGAAATGCAGAAGTAAAGAATGCAATGAAGAACTGTGGGGCAGAAATGTTTTCTTGA  
GGCTAAAGGGAAATAG (SEQ ID NO: 310)

20

**AOLFR169 sequences:**

MMDNHSSATEFHLLGFPGSQLHHLFAIFFFFYLVTLMGNTVIIIVCVDKRLQSPMYFFLSHL  
STLEILVTTHVPMMLWGLFLGCRQYLSLHVS LNFSCTMEFALLGVMAVDYVAVCNPLRY  
NIIMNSSTCIWVVIVSWVFGFLSEIWPIYATFQFTFRKSNSLDHFYCDRGQLKLSCDNTLLTEFI  
25 LFLMAVFILIGSLIPTIVSYTHIISTILKIPSASGRRKAFSTFASHFTCVVIGYGSCLFLYVKPKQTQ  
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDGMKRCCQLKD (SEQ ID NO: 311)

ATGATGGACAACCACTCTAGTGCCACTGAATTCACCTTCTAGGCTTCCCTGGGTCCCAAG  
GACTACACCACATTCTTTTGTATATTCTTTTCTTCTATTTAGTGACATTAATGGGAAAC  
30 ACGGTCATCATTGTGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCCT  
CAGCCACCTCTCTACCCTGGAGATCCTGGTCACAACCATAATTGTCCCCATGATGCTTTGG  
GGATTGCTCTTCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCCTG  
TGGGACCATGGAGTTTGCATTACTTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTGT  
AACCCTTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTTGGGTGGTAATAGTGT  
35 CATGGGTGTTTGGATTTCTTTCTGAAATCTGGCCCATCTATGCCACATTTACGTTTACCTTC  
CGCAAATCAAATTCATTAGACCATTTTTACTGTGACCGAGGGCAATTGCTCAAACCTGTCCT  
GCGATAACACTCTTCTCACAGAGTTTATCCTTTTCTTAATGGCTGTTTTTATTCTCATTGGT  
TCTTTGATCCCTACGATTGTCTCCTACACCTACATTATCTCCACCATCCTCAAGATCCCGTC  
AGCCTCTGGCCGGAGGAAAGCCTTCTCCACTTTTGCCTCCCACTTCACCTGTGTTGTGATTG  
40 GCTATGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACACAGGGAGTTGAGTACAA  
TAAGATAGTTTCCCTGTGGTTTCTGTGTTAACCCCTTCCCTGAATCCTTTCATCTTTACTCT  
TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCCT  
GAAAGATTAG (SEQ ID NO: 312)

45 **AOLFR170 sequences:**

MSFTSLIPSLCFSLTLPFLFCYLSLLPFLSAFLFITRWLLAFLSLFSVSVPVSSVSSSMVLCLYLSVS  
ASPSVFCFSCMQGPILWIMANLSQPSEFVLLGFSSFGELQALLYGPFLMLYLLAFMGNTIIIVMVI  
ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSLLVPHKVITFTGCMVQFYFHFSLGSTSFLL  
TDMALDRFVAICHPLRYGTLMSRAMCVQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH  
50 FFDNEPFLQLSCSDTRLLEFWDLMALTFVLSSFLVTLISYGYIVTTVLRIPSASSCQKAFSTCG  
SHLTLVFIGYSSTIFLYVRPGKAHSVQVRKVVALVTSVLTLPFLNPFILTCNQTVKTVLQGMQ  
RLKGLCKAQ (SEQ ID NO: 313)

ATGTCTTTCACTTCTCTCATACCCTCACTCTGTTTCTCCTTGACTCTCCCATTCCTGTTTTGT  
55 TATCTTTCTTTATTGCCGTTTCTTTCTGCTTTTCTGTTTATCACTCGCTGGCTACTGCTTT  
CTCTCTCTATTCTCTGTCTCTGTCCCTGTTTCTTCTGTTTCAAGTTCATGGTTCTCTGTCTC

TATCTCTCTGTTTCTGCCTCTCCGTCTGTCTTTTGTCTCTTGCATGCAGGGCCCCATACTG  
TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGTCCTCTTGGGCTTCTCCTCCTTTGG  
TGAGCTGCAGGCCCTTCTGTATGGCCCTTCCTCATGCTTTATCTTCTCGCTTCATGGGAA  
ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTACTTCTTC  
5 CTGGGCAATTTTTCCCTGCTGGAGATCTTGGTAACCATGACTGCAGTGCCAGGATGCTCT  
CAGACCTGTTGGTCCCCCACAAGTCATTACCTTCACTGGCTGCATGGTCCAGTTCTACTTC  
CACTTTTCCCTGGGGTCCACCTCCTTCCTCATCTGACAGACATGGCCCTTGATCGCTTTGT  
GGCCATCTGCCACCCACTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGTCCAGCTG  
10 GCTGGGGCTGCCTGGGCAGCTCCTTTCTAGCCATGGTACCCACTGTCCTCTCCCGAGCTC  
ATCTTGATTACTGCCATGGCGACGTCATCAACCACTTCTTCTGTGACAATGAACCTCTCCTG  
CAGTTGTCATGCTCTGACACTCGCCTGTTGGAATTCTGGGACTTTCTGATGGCCTTGACCTT  
TGTCTCAGCTCCTTCTGGTGACCCTCATCTCCTATGGCTACATAGTGACCACTGTGCTGC  
GGATCCCCTCTGCCAGCAGCTGCCAGAAGGCTTCTCCACTTGCGGGTCTCACCTCACACT  
GGTCTTCATCGGCTACAGTAGTACCATCTTCTGTATGTCAGGCCTGGCAAAGCTCACTCT  
15 GTGCAAGTCAGGAAGGTGCTGGCCTTGGTGACTTCAGTTCTCACCCCTTTCTCAATCCCT  
TTATCCTTACCTTCTGCAATCAGACAGTTAAAACAGTGCTACAGGGGCAGATGCAGAGGCT  
GAAAGGCCTTTGCAAGGCACAAATGA (SEQ ID NO: 314)

**AOLFR171 sequences:**

20 MVGNLLIWVTTIGSPSLGSLMYFFLAYLSLMDAIYSTAMSPKLMIDLLCDKIAISLSACMGQLFI  
EHLGGAEVFLVVMAYDRYVAISKPLHYLNIMNRLVCILLVVMAMIGGFVHSVQIVFLYSLP  
ICGNVIDHSVCDMYPLELLCLDTYFIGLTVVANGGHCVMVFTFLLISCGVILNFKTYSQEER  
HKALPTCISHIIVVALVFVPCIFMYVRPVSNFDFKLMTVFYIITLMLNPLIYSLRQSEMKNAM  
KNLWCEKLSIVRKRVSPTLNIFIPSSKATNRR (SEQ ID NO: 315)

25 ATGGTGGGAAACCTCCTCATTTGGGTGACTACTATTGGCAGCCCCCTCCTTGGGCTCCCTAA  
TGTACTTCTTCTTGCCTACTTGTCACTTATGGATGCCATATATTCCACTGCCATGTCACCC  
AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTTCTTGTGAGCTTGCATGGGTC  
30 AGCTCTTCATAGAACACTTACTTGGTGGTGCAGAGGTCTTCTTTTGGTGGTGATGGCCTA  
TGATCGCTATGTGGCTATCTCTAAGCCGCTGCACTATTTGAACATCATGAATCGACTGGTT  
TGCATCCTTCTGTTGGTGGTGGCCATGATTGGAGGTTTTGTGCACTCTGTGGTTCAAATTGT  
CTTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT  
ACCCATTGTTGGAAGTGTGTGCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA  
TGGTGGAAATAATTTGTATGGTCATCTTTACCTTTCTGCTAATCTCCTGTGGAGTCATCCTAA  
35 ACTTCCTTAAACTTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCCA  
CATCATGTGGTTGCCCTCGTTTTTTGTTCCCTGTATTTTTATGTATGTTAGACCGTTTTCCA  
ACTTTCCCTTTGATAAAATTAATGACTGTGTTTTATTCAATTATCACACTCATGTTGAATCCT  
TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA  
AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCACACTGAACATATTTATCCTAGTTCTA  
40 AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

**AOLFR172 sequences:**

MAETLQLNSTFLHPNFFILTGFPGLGSAQTWLTLVFGPIYLLALLGNGALPAVVWIDSTLHQPM  
FLLAILAATDLGLATSIAPGLLAVLWLGPRSVPYAVCLVQMFFVHALTAMESGVLLAMACDR  
45 AAAIGRPLHYPVLVTKACVGYAALALALKAVAIVVPFLLVAKFEHFQAKTIGHTYCAHMAV  
VELVVGNTQATNLYGLALSLAISGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSSHICVIL  
AFYIPGLFSYLAHRFGHHTVPKPVHILLSNIYLLPPALNPLIYGARTKQIRDRLLETFTFRKSPL  
(SEQ ID NO: 317)

50 ATGGCAGAAACTCTACAACCTCAATTCCACCTTCTACACCCAAACTTCTTCATACTGACTG  
GCTTTCCAGGGCTAGGAAGTGCCAGACTTGGCTGACACTGGTCTTTGGGCCATTTATCT  
GCTGGCCCTGCTGGGCAATGGAGCACTGCCGGCAGTGGTGTGGATAGACTCCACACTGCA  
CCAGCCCATGTTTCTACTGTTGGCCATCCTGGCAGCCACAGACCTGGGCTTAGCCACATCT  
ATAGCCCCAGGGTTGCTGGCTGTGCTGTGGCTTGGGCCCCGATCTGTGCCATATGCTGTGT  
55 GCCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC  
CATGGCCTGTGATCGTGCTGCGCAATAGGGCGTCCACTGCACTACCCTGTCCTGGTCACC

AAAGCCTGTGTGGGTTATGCAGCCTTGGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC  
 CTTTCCCACTGCTGGTGGCAAAGTTTGGACACTTCCAAGCCAAGACCATAGGCCATACCTA  
 TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGGTAACACACAGGCCACCAACTTATA  
 TGGTCTGGCACTTTCACTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT  
 5 GGACTCATTGCCCATGCTGTGCTGCAGCTACCTACCCGGGAGGCCCATGCCAAGGCCTTTG  
 GTACATGTAGTTCTCACATCTGTGTCACTTCTGGCCTTCTACATACCTGGTCTCTTCTCCTAC  
 CTCGCACACCGCTTTGGTCATCACACTGTCCCAAAGCCTGTGCACATCCTTCTCTCCAACAT  
 CTACTTGCTGCTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCGCACCAAGCAGATC  
 AGAGACCGACTCCTGGAAACCTTCACATTCAAGAAAAAGCCCGTTGTAA (SEQ ID NO: 318)

10

**AOLFR173 sequences:**

MSHTNVTFHPAVFVLPGIPGLEAYHIWLSIPLCLIYITAVLGNSILIVVIVMERNLHVPMYFFLS  
 MLAVMDILLSTTVPKALAIFWLQAHNIAFDACVTQGGFFVHMMFVGESAILLAMAFDRFVAIC  
 APLRYTTVLTWPVVGRIALAVITRSFCIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV  
 15 NIWYGFSVPVIMVILDVILIAVSYSILRAVFRLPQDARHKALSTCGSHLCVILMFYVPSFFTLL  
 THHFRNIPQHVHILLANLYVAVPPMLNPIVYGVKTKQIREGVAHRFFDIKTWCCTSPGLS  
 (SEQ ID NO: 319)

ATGAGTCACACCAATGTTACCATCTTCCATCCTGCAGTTTTTGTCTTCTTGGCATCCCTGG  
 20 GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTTGCCTCATTTACATCACTGCAGTCC  
 TGGGAAACAGCATCCTGATAGTGGTTATTGTCAATGGAACGTAACCTTCATGTGCCCATGTA  
 TTTCTTCTCTCAATGCTGGCCGTCATGGACATCCTGCTGTCTACCACCACTGTGCCCAAGG  
 CCCTAGCCATCTTTTGGCTTCAAGCAGATAACATTGCTTTTGATGCCTGTGTCAACCAAGGC  
 TTCTTTGTCCATATGATGTTTGTGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATTCG  
 25 CTTTGTGGCCATTTGTGCCCCACTGAGATATACAACAGTGCTAACATGGCCTGTTGTGGGG  
 AGGATTGCTCTGGCCGTCATACCCGAAGCTTCTGCATCATCTTCCCAGTCATATTCTTGCT  
 GAAGCGGCTGCCCTTCTGCCTAACCAACATTGTTCTCTACTCCTACTGTGAGCATATTGGA  
 GTGGCTCGTTTAGCCTGTGCTGACATCACTGTAAACATTGGTATGGCTTCTCAGTGCCCAT  
 TGTCAATGGTCATCTTGGATGTTATCCTCATCGCTGTGTCTTACTCACTGATCCTCCGAGCAG  
 30 TGTTTCGTTTGCCTCCAGGATGCTCGGCACAAGGCCCTCAGCACTTGTGGCTCCACCT  
 CTGTGTCATCCTTATGTTTTATGTTCCATCCTTCTTTACCTTATTGACCCATCATTTTGGGCG  
 TAATATTCCTCAACATGTCCATATCTTGCTGGCCAATCTTTATGTGGCAGTGCCACCAATGC  
 TGAACCCCATTTGTCTATGGTGTGAAGACTAAGCAGATACGTGAGGGGTGTAGCCCACCGGTT  
 CTTTGACATCAAGACTTGGTGTGTACCTCCCCTCTGGGCTCATGA (SEQ ID NO: 320)

35

**AOLFR175 sequences:**

MHFLSQNDLNLINLIPHLCLHRHSVIAGFTIHRHMKIFNSPNSSTFTGFILLGFPCPREGQILLFV  
 LFTVVYLLTLMGNSIICAVHWDQRLHAPMYILLANFSFLEICYVTSTVPSMLANFLSDTKHSF  
 SGCFLQFYFFSLGSTECFFLAVMAFDRLAICRPLRYPTIMTRRLCTNLVNCWVLGFIWFLPI  
 40 VNISQMSFCGSRIDHFLCDPAPLLTLTCKKGPVIELVFSVLSPLPVFMLFLFVGSYALVVRVAVL  
 RVPSAAGRRAKAFSTCGSHLAVVSLFYGSVLVVMYGSPPSKNEAGKQKTVTLFYSVVTPLLNPVI  
 YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTTCCCAAAATGATTTAAATATAAATCTGATTCCCCATCTATGTTTGCACCG  
 45 TCATTCAAGTAATTGCTGGTGTCTTTACAATTACAGGCACATGAAAATCTTCAACAGCCCC  
 AGCAACTCCAGCACCTTCACTGGCTTCATCCTCCTGGGCTTCCCTTGCCCCAGGGAGGGGC  
 AGATCCTCCTCTTTGTGCTCTTCACTGTTGTTACCTCCTGACCTCATGGGCAATGGTTCC  
 ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCCTGCTCGCCA  
 ACTTCTCCTTCTTGGAGATATGTTATGTCACTCCACAGTCCCCAGCATGCTGGCCAACCTC  
 50 CTCTCTGACACCAAGATCATCTCGTTCTCTGGCTGCTTCTCCAGTTCTACTTTTCTTCTCC  
 TTGGGCTCTACAGAAATGCTTTTCTGGCAGTTATGGCATTGATCGATACCTTGCCATCTG  
 TCGGCCTCTACGCTATCCAACCATATGACCAGACGTCTCTGTACCAATCTTGTGGTCAATT  
 GCTGGGTAATTGGTTTCATCTGGTTCTTGATTCTATCGTCAACATCTCCCAAATGTCCTTC  
 TGTGGATCTAGGATTATTGACCACTTCCTATGTGACCCAGCTCCTCTTCTAACTCTCACTTG  
 55 CAAAAAAGGCCCTGTGATAGAGCTTGTCTTTTCTGTCTTAAGTCCTCTGCCTGTCTTTATGC  
 TCTTTCTCTTCATTGTGGGGTCCTATGCTCTGGTCTGAGAGCTGTGTTGAGGGTCCCTTCA

GCAGCTGGGAGAAGAAAGGCTTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT  
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCCAACCATCTAAGAATGAAGCTGGAAAGC  
AGAAGACTGTGACTCTGTTTTATTCTGTTGTTACCCCACTGCTTAACCCTGTGATATATAGT  
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTGGGGAACATAA (SEQ ID NO:  
5 322)

**AOLFR176 sequences:**

MFFIHSLVTSVFLTALGPQNRTMHFVTEFVLLGFHGQREMQSCFFSFILVLYLLTLLNGAIVC  
AVKLDRLHTPMYILLGNFAFLEIWYISSTVPNMLVNILSEIKTISFSGCFLQFYFFFSLGTTECF  
10 LSVMAYDRYLAICRPLHYPSIMTGKFCILVCVCWVGGLCYVPVILISQLPFCGPNIIDHLVCD  
PGPLFALACISAPSTELICYTFNSMIFGPFLSILGSYTLVIRAVLCIPSGAGRRTKAFSTCGSHLMV  
VSLFYGTLMVMYVSPTSNGNPMQKIIITLVYTAMTPFLNPLIYSLRNKDKMDALKRVLGLTVS  
QN (SEQ ID NO: 323)

15 ATGTTCTTTATTATTCACTCTTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCCAGAA  
CAGAACAATGCATTTTGTGACTGAGTTTGTCTCTCTGGGTTTCCATGGTCAAAGGGAGATG  
CAGAGCTGCTTCTTCTCATTCACTGTTCTCTATCTCCTGACACTGCTAGGGAATGGAGC  
TATTGTCTGTGCAGTGAAATTGGACAGGCGGCTCCACACACCCATGTACATCCTTCTGGGA  
AACTTTGCCTTTCTAGAGATCTGGTACATTTCTCTCCACTGTCCCAAACATGCTAGTCAATAT  
20 CCTCTCTGAGATTAACCACATCTCCTTCTCTGGTTGCTTCTCTGCAATTCTATTTCTTTTTTC  
ACTGGGTACAACAGAGTGTCTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC  
TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTGT  
ATGCTGGGTAGGCGGATTTCTCTGCTATCCAGTCCCTATTGTTCTTATCTCCCAACTCCCT  
TCTGTGGGCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCCATTTGTTTGCACCTGGC  
25 CTGCATCTCTGCTCCTTCCACTGAGCTTATCTGTTACACCTTCAACTCGATGATTATCTTTG  
GGCCTTCTCTCCATCTTGGGATCTTACACTCTGGTCATCAGAGCTGTGCTTTGTATTCCC  
TCTGGTGTGGTGAACCTAAAGCTTTCTCCACATGTGGGTCCCACTAATGGTGGTGTCTC  
TATTCTATGGAACCTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT  
GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTTAAATCCCTTATCTAT  
30 AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCCTGGGGTTAACAGTTAGC  
CAAACTGA (SEQ ID NO: 324)

**AOLFR177 sequences:**

MSFFFVDLRPMNRSATHIVTEFILLGFPGCWKIQIFLFLVLYVLTLLNGAIYAVRCNPLLH  
35 TPMYFLLGNFAFLEIWYVSSTIPNMLVNILSKTKAISFSGCFLQFYFFFSLGTTECLFLAVMAYD  
RYLAICHPLQYPAIMTVRFCGKLVSFCWLIGFLGYPIPIFYISQLPFCGPNIIDHFLCDMDPLMAL  
SCAPAPITECIFYTQSSLVLFFTSMYILRSYILLTAVFQVPSAAGRRTKAFSTCGSHLVVSLFYG  
TVMVMYVSPTYGIPTLLQKILTLVYSVTPLFNPLIYTLRNKDKMLALRNVLFGMRIRQNS  
(SEQ ID NO: 325)

40 ATGTCTTTCTTCTTTGTAGACTTAAGACCCATGAACAGGTCAGCAACACACATCGTGACAG  
AGTTTATTCTCTGGGATTCCCTGGTTGCTGGAAGATTCAGATTTTCTCTTCTCATTGTTT  
TTGGTGATTTATGTCTTGACCTTGCTGGGAAATGGAGCCATCATCTATGCAGTGAGATGCA  
ACCCACTACTACACACCCCATGTACTTTCTGCTGGGAAATTTTGCCTTCTTCTGAGATCTGG  
45 TATGTGTCTCCACTATTCCTAACATGCTAGTCAACATTCTCTCCAAGACCAAGGCCATCTC  
ATTTTCTGGGTGCTTCTCCAGTTCTATTTCTTCTTTTCACTGGGAACAACCTGAATGTCTCT  
TTCTGGCAGTAATGGCTTATGATCGATACCTGGCCATCTGCCACCCACTGCAGTACCCTGC  
CATCATGACTGTAAGGTTCTGTGGTAAGCTGGTGTCTTTCTGTTGGCTTATTGGATTCCTTG  
GATACCCAATTCCCATTTTCTACATCTCCCAACTCCCTTCTGTGGTCTTAATATCATTGAT  
50 CACTTCTGTGTGACATGGACCACTGATGGCTCTATCCTGTGCCCCAGCTCCCACTAAGT  
AATGTATTTTCTATACTCAGAGCTCCCTTGCTCTTTTCTACTAGTATGTACATTCTTCGA  
TCCTATATCCTGTTACTAACAGCTGTTTTTCAAGTCCCTTCTGCAGCTGGTTCGGAGAAAAG  
CCTTCTCTACCTGTGGTTCTCATTGTTGTGGTATCTCTTTTCTATGGGACAGTCATGGTA  
ATGTATGTAAGTCTACATATGGGATCCCAACTTTATTGCAGAAGATCCTCACACTGGTAT  
55 ATTCAGTAACGACTCCTCTTTTAACTCTGATCTATACTCTTCGTAATAAGGACATGAAA



CTCGCTCTGAGAAATGTCCTGTTTGAATGAGAATTCGTCAAAATTCGTGA (SEQ ID NO: 326)

**AOLFR178 sequences:**

5 MVGANHSVVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNSLILLTVTSDPHLHSPMYFLL  
ANLSFIDLGVSSVTSFKMIYDLFRKHEVISFGGCIAQIFFIHVIGGVEMVLLIAMAFDRYVAICKP  
LQYLTIMSPRMCMMFFLVAAWVTGLIHSVVQLVFVNLPFCGPNVSDSFYCDLPRFIKLACTDSY  
RLEFMVTANSFISLGSFFILISYVVILTVLKHSSAGLSKALSTLSAHVSVVVLFPGPLIFVYTW  
PSPSTHLDKFLAIFDAVLTPVLNPIIYTFRN (SEQ ID NO: 327)

10 ATGGTTGGGGCAAATCACTCCGTGGTGTGAGAGTTTGTGTTCTCCTGGGACTCACCAATTCTCT  
GGGAGATCCGACTTCTCCTCCTTGTGTTCTCCTCCATGTTTACATGGCCAGTATGATGGGA  
AACTCTCTCATTTTGTCTACTGTGACTTCTGACCCTCACTTGCCTCCCCATGTATTTCT  
GTTAGCCAACCTCTCCTTCATTGACCTGGGTGTTTCTCTGTCACTTCTCCCAAATGATTT  
15 ATGACCTGTTTACAGAAAGCACGAAGTCATCTCCTTTGGAGGCTGCATCGCTCAAATCTTCTT  
CATCCACGTCATTGGCGGTGTGGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAT  
GTGGCCATATGTAAGCCCCTCCAGTACCTGACCATTATGAGCCCAAGAATGTGCATGTTCT  
TCTTAGTGGCTGCCTGGGTGACCGGCCTTATCCACTCTGTAGTTCAATTGGTTTTTGTAGTA  
AACTTGCCCTTCTGTGGTCCATAATGTATCGGACAGCTTTTACTGTGACCTTCTCGGTTTCT  
20 CAACTTGCTGTCACAGACAGCTACCGACTGGAGTTCATGGTTACAGCCAACAGTGGATTCT  
ATCTCTCTGGGCTCCTTCTTCTACTGATCATTTCCTATGTGGTTCATCATTCTCACTGTTCT  
GAAACACTCTTCACTGGTTTATCCAAGGCTCTGTCCACCCTTTCAGCTCACGTCAGTGTG  
GTAGTTTGTCTTGGTCTTTGATTTTGTCTATACGTGGCCATCTCCCTCCACACACCT  
GGATAAGTTTCTGGCCATCTTTGATGCAGTTCTCACTCCTGTTTTAAATCCTATCATCTACA  
25 CATTCAAGGAATTGA (SEQ ID NO: 328)

**AOLFR179 sequences:**

MNGMNHSVVSEFVFMGLTNSREIQLLLFFVSLLFYFASMMGNLVIVFTVTMDAHLHSPMYFLL  
ANLSIIDMAFCSITAPKMICDIFKKHKAISFRGCITQIFFSHALGGTEMVLLIAMAFDRYMAICKP  
30 LHYLTIMSPRMCCLYFLATSSIIHLISLVQLVFVVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEL  
EFMVTVNISGLISVGSFVLLVISYIFILFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFFYTW  
PSPSTHLDKFLAIFDAFITPFLNPVIYTFRNKDMKVAMRRLCSRLAHFTKIL (SEQ ID NO: 329)

35 ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTCATGGGACTCACCAACTCAC  
GGGAGATTACGCTTCTACTTTTTGTTTTCTCTTTGTTGTTCTACTTTGCGAGCATGATGGGA  
AACCTTGTCAATTGTATCACTGTAACCATGGATGCTCATCTGCCTCCCCATGTATTTCTCT  
CCTGGCTAACCTCTCAATCATTGATATGGCATTGTTGCTCAATTACAGCCCCTAAGATGATTT  
GTGATATTTTCAAGAAGCACAAAGCCATCTCCTTTGCGGGATGTATTACTCAGATCTTCTT  
TAGCCATGCTCTTGGGGGCACTGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAC  
40 ATGGCCATATGTAAACCTCTCCACTACCTGACCATCATGAGCCCAAGAATGTGTCTATACT  
TTTTAGCCACTTCTCTATCATTGGCCTTATCCACTCATTGGTCCAATTAGTTTTTGTGGTA  
GATTTACCTTTTTGTGGTCCATAATATCTTTGACAGTTTTTACTGTGATCTCCCTCGGCTCCT  
CAGACTTGCTGTACCAACACCCCAAGAACTGGAGTTCATGGTCACTGTCAATAGTGGACTC  
ATTTCTGTGGGCTCCTTTGTCTTGTGTAATTTCTACATCTTCATTCTGTTCCTGTTTG  
45 GAAACATTCTTCTGGTGGTCTAGCCAAGGCCCTCTTACCCTGTCAGCTCATGTCACTGTG  
GTCATCTTGTCTTTGGGCCACTGATGTTTTTCTACACATGGCCTTCTCCACATCACACCT  
GGATAAATATCTTGCTATTTTTGATGCATTTATTACTCCTTTTCTGAATCCAGTTATCTACA  
CATTCAAGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCAGTCGTCTTGCGCATT  
TTACAAAGATTTTGTA (SEQ ID NO: 330)

50

**AOLFR180 sequences:**

MTNKMYAIYIKNLNYFSFLIVQCLQPTMAIFNNTTSSSSNFLTAFPGLECAHVWISIPVCCLYTI  
ALLGNSMIFLVITKRRHLKPMYYFLSMLAAVDLCLTITTLPTVLGVLFHAREISFKACFIQMF  
FVHAFSLLESSVLVAMAFDRFVAICNPLNYATILTDRMVLVIGLVICIRPAVFLPLLVAINTVSF  
55 HGGHELHPFCYHPEVIKYTYSKPWISSFWGLFLQLYLNGLDVLFILFSYVLILRTVLGIVARKK

QKALSTCVCHICAVTIFYVPLISLSLAHRLFHSTPRVLCSTLANIYLLLPPVLNPIIYSLKTKTIR  
QAMFQLQSKGSWGFNVRGLRGRWD (SEQ ID NO: 331)

5 ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTCTTTCCTCATAGT  
TCAGTGTCTTCAACCAACCATGGCAATATTCAATAACACCACTTCGTCTTCCTCAAACCTCC  
TCCTCACTGCATTCCCTGGGCTGGAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT  
CTCTACACCATTGCCCTCTTGGGAAACAGTATGATCTTTCTTGTCATCATTACTAAGCGGA  
GACTCCACAAACCCATGTATTATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC  
ATTACGACCCTTCCCCTGTGCTTGGTGTCTCTGGTTTCATGCCCCGGGAGATCAGCTTTAA  
10 AGCTTGCTTCATTCAAATGTTCTTTGTGCATGCTTTCTCCTTGCTGGAGTCCCTCGGTGCTGG  
TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCCACTGAACTATGCTACTATCCCTC  
ACAGACAGGATGGTCCCTGGTGATAGGGCTGGTCATCTGCATTAGACCAGCAGTTTCTTAC  
TTCCCCTTCTTGATGCCATAAACACTGTGTCTTTTCATGGGGGTACAGAGCTTTCCCATCCA  
TTTGTCTACCAACCCAGAGTGATCAAATACACATATTCCAAACCTTGGATCAGCAGTTTTT  
15 GGGGACTGTTTCTTCAGCTCTACCTGAATGGCACTGACGTATTGTTTATTCTTTTCTCTAT  
GTCCTGATCCTCCGTACTGTTCTGGGCATTGTGGCCCGAAAGAAGCAACAAAAAGCTCTCA  
GCACTTGTGTCTGTACATCTGTGCAGTCACTATTTTCTATGTGCCACTGATCAGCCTCTCT  
TTGGCACACCGCCTCTTCCACTCCACCCCAAGGGTGCTCTGTAGCACTTTGGCCAATATTTA  
TCTGCTCTTACCACCTGTGCTGAACCTATCATTTACAGCTTGAAGACCAAGACAATCCGC  
20 CAGGCTATGTTCCAGCTGCTCCAATCCAAGGGTTCATGGGGTTTTAATGTGAGGGGTCTTA  
GGGGAAGATGGGATTGA (SEQ ID NO: 332)

**AOLFR181 sequences:**

MSVLNNSEVKLFLLIGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIIKTEPSLHEPMYYFLAML  
25 AVSDMGLSLSSLPTMLRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLIMSLDRFLAIHNPLR  
YSSILTSNRVAKMGLILAIRSILLVIPFPFTLRRLKYCQKNLLSHSYCLHQDTMKLACSDNKTNV  
IYGFIALCTMLDLALIVLSYVLILKTIISIASLAERLKALNTCVSHICAVLTFYVPIITLAAMHFF  
AKHKSPVLVILIADMFLVPLMNPVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

30 ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCTCTGATTGGGATCCCAGGACTGG  
AACATGCCCACATTTGGTTCTCCATCCCCATTTGCCTCATGTACCTGCTTGCCATCATGGGC  
AACTGCACCATTCTCTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATTT  
CCTTGCCATGTTGGCTGTCTCTGACATGGGCCTGTCCCTCTCCTCCCTTCTACCATGTTGA  
GGGTCTTCTTGTTCAATGCCATGGGAATTTACCTAATGCCTGCTTGTCTCAAGAATTCTTC  
35 ATTCATGGATTCACTGTCTGATGGAATCCTCAGTACTTCTAATTATGTCTTTGGACCGCTTCT  
TGCCATTACAATCCCTTAAGATACAGTTCTATCCTCACTAGCAACAGGGTTGCTAAAATG  
GGACTTATTTTAGCCATTAGGAGCATTCTCTTAGTGATTCCATTTCCCTTCACCTTAAGGAG  
ATAAAATATTGTCAAAAGAATCTTCTTTCTCACTCATACTGTCTTCATCAGGATACCATGA  
AGCTGGCCTGCTCTGACAACAAGACCAATGTCTATGGCTTCTTCATTGCTCTCTGTACT  
40 ATGCTGGACTTGGCACTGATTGTTTGTCTTATGTGCTGATCTTGAAGACTATACTCAGCAT  
TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGTCTCCACATCTGTGTGTG  
CTCACCTTCTATGTGCCCATCATCACCTGGCTGCCATGCATCACTTTGCCAAGCACAAAA  
GCCCTCTTGTTGTGATCCTTATTGCAGATATGTTCTTGTGGTGCCGCCCTTATGAACCCC  
ATTGTGTACTGTGTAAAGACTCGACAAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAAT  
45 GTATGTGGGAGATAA (SEQ ID NO: 334)

**AOLFR182 sequences:**

MTLGS LGNSSSVSATFLLSGIPGLERMHIWISIPCFMYLVSIPGNCTILFIIKTERSLHEPMYLFL  
SMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFFIHCFSFLESSVLLSMAFDRFVAICHP  
50 LHYVSILNTVIGRIGLVSLGRSVLIFPLPFMLKRFPYCGSPVLSHSYCLHQEVMKLACADMK  
ANSIYGMFVIVSTVGIDSLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV  
IHRFGKQAPHLVQVVMGFMYLLFPPVMNPVYSVKTKQIRDRVTHAF CY (SEQ ID NO: 335)

ATGACCCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCTGCTGAGTG  
55 GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCACTGTGCTTCATGTATCT  
GTTTCCATCCCGGGCAACTGCACAATTCTTTTATCATTAACAGAGCGCTCACTTCAT

GAACCTATGTATCTCTTCTGTCCATGCTGGCTCTGATTGACCTGGGTCTCTCCCTTTGCAC  
TCTCCCTACAGTCCTGGGCATCTTTTGGGTGGAGCACGAGAAATTAGCCATGATGCCTGC  
TTTGCTCAGCTCTTTTTCATTCACTGCTTCTCCTTCTCGAGTCCTCTGTGCTACTGTCTATG  
5 GCCTTTGACCGCTTTGTGGCTATCTGCCACCCCTTGCACTATGTTTCCATTCTCACCAACAC  
AGTCATTGGCAGGATTGGCCTGGTCTCTCTGGGTCGTAGTGTAGCACTCATTTTCCATTA  
CCTTTTATGCTCAAAAGATTCCCCTATTGTGGCTCCCCAGTTCTCTCACATTCTTATTGTCT  
CCACCAAGAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT  
GTTTGTCACTGCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTCTCTTATGCTCTGA  
10 TCCTGCGCACCGTGTGTCCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG  
TGTTTCCCACATCTGTGCTGTGCTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTCATCC  
ATCGCTTTGGAAAGCAGGCACCCACCTGGTCCAGGTGGTCATGGGTTTCATGTATCTTCT  
CTTCTCTCTGTGATGAATCCCATTGTCTACAGTGTGAAGACCAAACAGATCCGGGATCGA  
GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

15 **AOLFR183 sequences:**

MTNLNASQANHRNFILTGIPGTPDKNPWLAFPLGFLYTLTLLNGTILAVIKVEPSLHEPTYFFL  
SILALTDVLSMSTLPSMLSIYWFNAPQIVFDACIMQMFFIHVFGIVESGVLVSMADFDRFVAIRN  
PLHYVSILTHDVIRKGTGISVLTRAVCVFPVPFLIKCLPFCHSNVLSHSYCLHQNMMLACASTR  
20 INSLYGLIVIFTLGLDVLLTLLSYVLTLKTVLGIVSRGERLKTLSLCLSHMSTVLLFYVPMFGA  
ASMIHRFWEHLSPVVMVMADIYLLPVLNPIVYSVKTKQI (SEQ ID NO: 337)

ATGACGAACCTGAATGCATCACAGGCCAACACCGTAACCTTCATTCTGACAGGTATCCCAG  
GAACGCCAGACAAGAACCCATGGTTGGCCTTCCCTGGGATTTCTCTACACACTCACT  
25 CCTGGGAAATGGTACCATCCTAGCTGTCAAGGTGGAGCCAAGTCTCCATGAGCCACG  
TATTACTTCCTTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCCTCC  
ATGCTCAGCATCTACTGGTTTAATGCCCTCAGATTGTTTTTGATGCATGCATCATGCAGAT  
GTTCTTCATCCATGTATTTGGAATAGTAGAATCAGGAGTCCTAGTGTCCATGGCCTTTGAC  
AGATTTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTCAGATGTTATTG  
AAAGACTGGAATATCTGTCTCACCCTGGGAGTCTGTGTGGTATTCCCTGTGCCCTTCCTT  
30 ATAAAGTGCCTACCCTTCTGCCATCCAATGTCTTGTCTCATTACATACTGTCTTACCAAAA  
CATGATGCGGCTAGCTTGTGCCAGCACCCGCATCAACAGCCTCTACGGCCTCATCGTCGTC  
ATCTTCACACTGGGGCTCGATGTTCTCCTCACTCTACTGTCTTATGTACTCACCTGAAGAC  
TGTGCTGGGCATTGTCTCCAGAGGTGAAAGGCTGAAAACCCTCAGCACATGCCTCTCTCAC  
ATGTCTACCGTGCTCCTCTTCTATGTTCTTTTATGGGTGCTGCCTCCATGATCCACAGAT  
35 TTGGGAGCATTTATCACCAGTAGTGCACATGGTCATGGCTGATATATACCTACTGCTCCCG  
CCTGTGCTAAACCCCATTTGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

**AOLFR184 sequences:**

MSTLPTQIAPNSSTSMAPTFLLVGMPGLSGAPSWWTLPLIAVYLLSALGNGTILWIALQPALHR  
40 PMHFFLLSVSDIGLVTALMPTLLGIALAGAHTVPASACLLQMVFHVFVSMESSVLLAMSID  
RALAICRPLHYPALLTNGVISKISLAISFRCLGLHLPLPFLLAYMPYCLPQVLTHSYCLHPDVARL  
ACPEAWGAAAYSLFVVLAMGLDPLLIFFSYGLIGKVLQGVESREDRWKAGQTCAAHLSAVLLF  
YIPMILLALINHPPELITQHTHTLLSYVHFLPLINPILYSVKMKEIRKRLNRLQPRKVGAQ  
(SEQ ID NO: 339)

45 ATGTCAACATTACCAACTCAGATAGCCCCAATAGCAGCACTTCAATGGCCCCCACCTTCT  
TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCCTCCTGGTGGACATTGCCCTCATTGC  
TGCTACCTTCTCTGCACTGGGAAATGGCACCATCCTCTGGATCATTGCCCTGCAGCCC  
GCCCTGCACCGCCCAATGCACTTCTTCTCTTCTGCTTAGTGTGTGATATTGGATTGGT  
50 CACTGCCCTGATGCCACACTGCTGGGCATCGCCCTTGTCTGCTGCTCACATGCTCCTGCC  
TCAGCCTGCCTTCTACAGATGGTTTTATCCATGTCTTTTCTGTGATGGAGTCTCTGTCTT  
GCTCGCCATGTCCATTGATCGGGCACTGGCCATCTGCCGACCTCTCCACTACCCAGCGCTC  
CTCACCAATGGTGTAATTAGCAAAATCAGCCTGGCCATTTCTTTTCGATGCCTGGGTCTCC  
ATCTGCCCTGCCATTCCTGCTGGCCTACATGCCCTACTGCCTCCCACAGGTCCTAACCCAT  
55 TCTTATTGCTTGCATCCAGATGTGGCTCGTTTGGCCTGCCGAGAAGCTTGGGGTGCAGCCT  
ACAGCCTATTTGTGGTTCTTTCAGCCATGGGTTTGGACCCCTGCTTATTTCTTCTCTAT

GGCCTGATTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGCTGGT  
CAAACCTGTGCTGCCACCTCTCTGCAGTGCTCCTCTTCTATATCCCTATGATCCTCCTGGC  
ACTGATTAACCATCCTGAGCTGCCAATCACTCAGCATACCCATACTCTTCTATCCTATGTCC  
ATTTCTTCTTCTCCTCCATTGATAAACCTATTCTCTATAGTGTCAAGATGAAGGAGATTAGA  
5 AAGAGAATACTCAACAGGTTGCAGCCCAGGAAGGTGGGTGGTGCTCAGTGA (SEQ ID NO:  
340)

**AOLFR185 sequences:**

MFYPILNDISTKNNSNIMSCCNILFIKTVEIILVYNQTSQSPWYPIVPSKSLVYNNNTCFDCYHLQR  
10 VDCVPSRDHINQSMVLASGNSSSHPVSFILLGIPGLESFQLWIAFPFCATYAVAVVGNITLLHVIR  
IDHTLHEPMYLFLAMLAITDLVLSSSTQPKMLAIFWFHAHEIQYHACLIQVFFIHAFSSVESGVL  
MAMALDCYVATCFPLRHSSILTPSVVIKLGTIVMLRGLLWVSPFCFMVSRMPFCQHQAIPQSYC  
EHMAVLKLVCADTISRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA  
SHICVILALYIPALFSFLTFRFGHDVPRVVHILFANLYLLIPMLNPIHYGVRTKQIGDRVIQGCCG  
15 NIP (SEQ ID NO: 341)

ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTCATGTT  
GTAACATATTATTTATTTAAAACAGTTGAAATTATCTAGTTTATAATCAAACCCAATCACC  
20 CTGGTATCCAATAGTCCCATCCAAAAGCCTTGATATAATAATAACACTTGTTTTGATTGTT  
ATCATCTGCAGAGAGTAGATTGCGTTCCCAGCAGAGACCATATTAACCAAGTCCATGGTGCT  
GGCTTCAGGGAACAGCTCTTCTCATCCTGTGTCTTCTCATCCTGCTTGGAATCCCAGGCCTG  
GAGAGTTTCCAGTTGTGGATTGCCTTTCCGTTCTGTGCCACGTATGCTGTGGCTGTTGTTGG  
AAATATCACTCTCCTCCATGTAATCAGAATTGACCACACCCCTGCATGAGCCCATGTACCTC  
TTTCTGGCCATGCTGGCCATCACTGACCTGGTCTCTCCTCCTCCACTCAACCTAAGATGTT  
25 GGCCATATTCTGGTTTCATGCTCATGAGATTCAGTACCATGCCTGCCTCATCCAGGTGTTCT  
TCATCCATGCCTTTTCTTCTGTGGAGTCTGGGGTGCTCATGGCTATGGCCCTGGACTGCTAC  
GTGGCTACCTGCTTCCCACTCCGACACTCTAGCATCCTGACCCCATCGGTGCTGATCAAAC  
TGGGGACCATCGTGATGCTGAGAGGGCTGCTGTGGGTGAGCCCCTTCTGCTTCATGGTGTC  
TAGGATGCCCTTCTGCCAACACCAAGCCATTCCCCAGTCATACTGTGAGCACATGGCTGTG  
30 CTGAAGTTGGTGTGTGCTGATACAAGCATAAGTCGTGGGTATGGGCTCTTTGTGGCCTTCT  
CTGTGGCTGGCTTTGATATGATTGTCATTGGTATGTCATACGTGATGATTTTGAGAGCTGT  
GCTTCAGTTGCCCTCAGGTGAAGCCCGCCTCAAAGCTTTTAGCACACGTGCCTCCCATATC  
TGTGTCATCTTGGCTCTTTATATCCCAGCCCTTTTTCTTTCTTCTCACCTACCGCTTTGGCCAT  
GATGTGCCCCGAGTTGTACACATCCTGTTTGCTAATCTCTATCTACTGATACCTCCCATGCT  
35 CAACCCCATCATTTATGGAGTTAGAACCAAACAGATCGGGGACAGGGTTATCCAAGGATG  
TTGTGGAAACATCCCCTGA (SEQ ID NO: 342)

**AOLFR186 sequences:**

MSNASLVTAFILTGLPHAPGLDALLFGIFLVVYVLTVLGNLILLVIRVDSHLHTPMYYFLTNLS  
40 FIDMWFSVTVPKMLMTLVSPSGRAISFHSVAQLYFFHFLGSTECFLYTVMSYDRYLAIISYPL  
RYTSMMSGSRCALLATGTWLSGSLHSAVQILTFLHPYCGPNQIQHYFCDAPPILKLACADTSA  
NVMVIFVDIGIVASGCFVLIVLSYVSIVCSILRIRTS DGRRRAFQTCASHCIVVLCFFVPCVVIYLR  
PGSMDAMDGVVAIFYTVLTPLLNPVYTLRNKEVKKAVLKL RDKVAHPQRK (SEQ ID NO:  
343)

ATGTCCAACGCCAGCCTCGTGACAGCATTATCCTCACAGGCCTTCCCCATGCCCCAGGGC  
TGGACGCCCTCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT  
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCTCTCA  
CCAACCTGTCTTCATTGACATGTGGTTCTCCACTGTACGGTGCCCCAAATGCTGATGAC  
50 CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTT  
TCCACTTCTGGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCTCTATGATCGCTACTG  
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGGTGTGCCCTCCTGG  
CCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT  
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA  
55 AACTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTCATCTTTGTGGACATTGGGATAGT  
GGCCTCAGGCTGCTTTGTCCTGATAGTGCTGTCCTATGTGTCCATCGTCTGTTCCATCCTGC

GGATCCGCACCTCAGATGGGAGGCGCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATTGT  
GGTCCTTTGCTTCTTTGTTCCCTGTGTTGTCAATTTATCTGAGGCCAGGCTCCATGGATGCCA  
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACGCCCCCTTCTCAACCCTGTTGTGTAC  
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTTAGAGACAAAGTAGCACAT  
5 CCTCAGAGGAAATAA (SEQ ID NO: 344)

**AOLFR187 sequences:**

MAQVRALHKIMALFSANSIGAMNNSDTRIAGCFLTGIPGLEQLHIWLSIPFCIMYIAALEGNGLI  
CVILSQAILHEPMYIFLSMLASADVLLSTTMPKALANLWLGYSHISFDGCLTQKFFIHFLEHSA  
10 VLLAMAFDRYVAICSPRYVTILTSKVIGKIVTATLSRSFIIMFPSIFLEHLHYCQINIIAHTFCEH  
MGIAHLSCSDISINVWYGLAAALLSTGLDIMLITVSYIHILQAVFRLLSQDARSKALSTCGSHICV  
ILLFYVPALFSVFAYRFGGRSIPCYVHILLASLYVVIPMLNPVIYGVRTKPILEGAKQMFSNLAK  
GSK (SEQ ID NO: 345)

15 ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG  
CTATGAACAACCTCTGACACTCGCATAGCAGGCTGCTTCCTCACTGGCATCCCTGGGCTGGA  
GCAACTACATATCTGGCTGTCCATCCCCTTCTGCATCATGTACATCGCTGCCCTGGAAGGC  
AATGGCATCCTAATTTGTGTCACTCTCCAGGCAATCCTGCATGAGCCCATGTACATAT  
TCTTATCTATGCTGGCCAGTGCTGATGTCTTGCTCTCTACCACCACCATGCCTAAGGCCCTG  
20 GCCAATTTGTGGCTAGGTTATAGCCACATTTCTTTGATGGCTGCCTCACTCAAAAGTTCTT  
CATTCACTTCCTCTTCATTCACTCTGCTGTCTGCTGGCCATGGCCTTTGACCGCTATGTGG  
CCATCTGCTCCCCCTGCGATATGTCACAATCCTCACAAAGCAAGGTCATTGGGAAGATCGT  
CACTGCCACCCTGAGCCGAGCTTCATCATTATGTTTCCATCCATCTTTCTCCTTGAGCACC  
TGCACATTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATTGCCCA  
25 TCTGTCTGTTCTGATATCTCCATCAATGTCTGGTATGGGTGGCAGCTGCTCTTCTCTCCA  
CAGGCCTGGACATCATGCTTATTACTGTTTCTACATCCACATCCTCCAAGCAGTCTTCCGC  
CTCCTTTCTCAAGATGCCCCGCTCCAAGGCCCTGAGTACCTGTGGATCCCATATCTGTGTCAT  
CCTACTCTTCTATGTCCCTGCCCTTTTTTCTGTCTTTGCCTACAGGTTTGGTGGGAGAAGCA  
TCCCATGCTATGTCCATATTCTCCTGGCCAGCCTCTACGTTGTCATTCCCTCCTATGCTCAAT  
30 CCCGTTATTTATGGAGTGAGGACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTTCA  
AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

**AOLFR188 sequences:**

MFPSLPCPVLLVQLPLMNENMQCFVFCSDSLLRMMVSRFIHVPFVKMKRIIVGGYSKHFFSN  
35 ELLCVRPWSGKTWSIRHHIFDMELLTNNLKFITDPFVCRLRHLSPTPSEEHMKNKNNVTEFILL  
GLTQNPEGQKVLVFTLLIYMVTIMGNLLIIVTIMASQSLGSPMYFFLASLSFIDTVYSTAFAPK  
MIVDLLSEKKTISFQGCMAQLFMDHLFAGAIEVLLVVMAYDRYMAICKPLHELITMNRRCVCL  
MLLAAWIGGFLHSLVQFLFIYQLPFCGPNVIDNFLCDLYPLLKLACTNTYVTGLSMIANGGAIC  
AVTFFITILLSYGVILHSLKTQSLEGRKAFYTCASHVTVVILFFVPCIFLYARPNSTFPIDKSMTV  
40 VLTFITPMLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)

ATGTTCCCTCCCTGTGTCCATGTGTTCTCCTTGTTCAACTCCCACTTATGAATGAGAACAT  
GCAGTGTTTTGTTTTCTGTTCTTGTGATAGTTTGTGAGAAATGATGGTTTCCCGCTTCATCC  
ATGTCCCATTGTGAAAAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTTC  
45 TAATGAGCTGCTCTGTGTGAGGCCCTGGTCAGGGAAAACGTGGTCGATAAGGCATCACAT  
TTTGACATGGAGCTTCTGACAAATAATCTCAAATTTATCACTGACCCTTTTGTGTAGGC  
TCCGACACCTGAGTCCAACACCTTCAGAAGAACACATGAAAAATAAGAACAATGTGACTG  
AATTTATCCTCTTAGGGCTCACACAGAACCTGAGGGGCAAAAGGTTTTATTGTACATT  
CTTACTAATCTACATGGTGACGATAATGGGCAACCTGCTTATCATAGTGACCATCATGGCC  
50 AGCCAGTCCCCTGGGTCCCCCATGTACTTTTTCTGGCTTCTTTATCATTATAGATACCGT  
CTATTCTACTGCATTTGCTCCCCAAATGATTGTTGACTTGCTCTCTGAGAAAAAGACCATT  
CCTTTAGGGTTGTATGGCTCAACTTTTTATGGATCATTTATTTGCTGGTGCTGAAGTCATT  
CTTCTGGTGGTAATGGCCTATGATCGATACATGGCCATCTGTAAGCCTCTTCATGAATTGA  
TCACCATGAATCGTCGAGTCTGTGTTCTTATGCTGTTGGCGGCCTGGATTGGAGGCTTTCT  
55 TCACTCATTGGTTCAATTTCTTTATTTATCAGCTCCCTTTCTGTGGACCCAATGTCATTG  
ACAACCTCCTGTGTGATTGTATCCCTTATTGAACTTGCTTGACCAATACCTATGTCACT

GGGCTTTCTATGATAGCTAATGGAGGAGCGATTTGTGCTGTACCTTCTTCACTATCCTGC  
 TTTCTATGGGGTCAATTACACTCTCTTAAGACTCAGAGTTTGGAAAGGAAACGAAAAGC  
 TTTCTACACCTGTGCATCCACGTCACCTGTGGTCATTTTATTCTTTGTCCCCTGTATCTTCTT  
 GTATGCAAGGCCCAATTCTACTTTTCCCATTGATAAATCCATGACTGTAGTTCTAACTTTTA  
 5 TAACTCCCATGCTGAACCCACTAATCTATACCCTGAAGAATGCAGAAATGAAAAGTGCCAT  
 GAGGAACTTTGGAGTAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA  
 (SEQ ID NO: 348)

**AOLFR189 sequences:**

10 MQQNNVPEFILLGLTQDPLRQKIVFVIFLIFYMGTVVGNMLIIVTIKSSRTLGSMPYFFLYLSF  
 ADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFALHLFGCMEIFVLILMAVDYVAICKPLRYP  
 TIMSQQVCILIVLAWIGSLIHSTAQIILALRLPFCGPYLDHYCCDLQPLLKLACMDTYMINLLL  
 VSNPGAICSSSFMIISYIVILHSLRNHSAKGKKKALSACTSHIIVVILFFGPCIFIYTRPPTTFPMD  
 KMVAVFYTIGTLPFLNPLYTSEECRSEKCHEK (SEQ ID NO: 349)

15 ATGCAGCAAAATAACAGTGTGCCTGAATTCATACTGTTAGGATTAACACAGGATCCCTTGA  
 GGCAGAAAATAGTGTGTAATCTTCTTAATTTTCTATATGGGAACTGTGGTGGGGAATAT  
 GCTCATTATTGTGACCATCAAGTCCAGCCGGACACTAGGAAGCCCCATGACTTCTTTCTA  
 TTTTATTTGTCCCTTGCAGATTCTTGCTTTTCAACTCCACAGCCCCCTAGATTAATTGTGGA  
 20 TGCTCTCTCTGAAAAGAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTTCACATA  
 CATTTATTTGGCTGCATGGAGATCTTTGTCCTCATTCTCATGGCTGTTGATCGCTATGTGGC  
 CATCTGTAAGCCCTTGCCTTACCCAACCATCATGAGCCAGCAGGTCTGCATCATCCTGATT  
 GTTCTTGCCTGGATAGGGTCTTTAATACACTCTACAGCTCAGATTATCCTGGCCTTAAGATT  
 GCCTTTCTGTGGACCCCTATTTGATTGATCATTATTGCTGTGATTGTCAGCCCTTGTGAAAC  
 25 TTGCCTGCATGGACACTTACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTTG  
 CTCAAGTAGTTTCATGATTTTGATAATTTTCATATATTGTCATCTTGCATTCACTGAGAAACC  
 ACAGTGCCAAAGGGAAGAAAAAGGCTCTCTCCGCTTGACGTCTCACATAATTGTAGTCAT  
 CTTATTCTTTGGCCCATGTATATTCATATATACACGCCCCCGACCACTTTCCCCATGGACA  
 AGATGGTGGCAGTATTTTATACTATTGGAACACCCTTTCTCAATCCACTCATCTACACATCT  
 30 GAGGAATGCAGAAGTGAAAAATGCCATGAGAAAG (SEQ ID NO: 350)

**AOLFR190 sequences:**

MQRSNHTVTVEFILLGFTTDPGMQLGLFVVLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN  
 LSFLDLWYSSVHTPKILVTCISEDKSISFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL  
 35 YAQTMPRRLCICLVLYSYTGGFVNAILTSNTFTLDFCGDNVIDDFCDVPLVLKACSVRESYQ  
 AVLHFLLASNVISPTVLILASYLSIITILRIHSTQGRJKVFSTCSSHLISVTLYYGSILYNYSRPSS  
 YSLKRDKMVSTFYTMLFPMLNPMIYSLRSKDKMDALKKFFKSA (SEQ ID NO: 351)

ATGCAGAGGAGCAATCACACAGTGACTGAGTTCATCCTGCTGGGCTTCACCACAGATCCAG  
 40 GGATGCAACTGGGCCTCTTTGTGGTGTTCCTGGGTGTGTACTGTCTGACTGTGGTAGGAAG  
 TAGCACCCCTCATCGTGTGATCTGTAATGACTCCCGCCTACACACACCCATGTATTTGTCA  
 TTGGAAATCTGTCATTTCTGGATCTCTGGTATTCTTCTGTCCACACCCCAAAGATCCTAGTG  
 ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTGTCAGTTCTTCTCTGC  
 CAGGCTGGCCTATAGTGAGTGCTACCTACTGGCTGCCATGGCTTATGACCACTACGTGGCC  
 45 ATCTCCAAGCCCTGCTTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTTGGTTTT  
 ATATTCTATACTGGGGGTTTTGTCAATGCAATAATATTAACCAGCAACACATTACATTG  
 GATTTTTGTGGTGACAATGTCATTGATGACTTTTTCTGTGATGTTCCACCCCTCGTGAAGCT  
 GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCCTTCTGGCCTCCAATGTC  
 ATCTCCCCTACTGTGCTCATCTTGGCTCTTACCTCTCCATCATCACCACCACTCAGGAT  
 50 CCACTCTACCCAGGCCGCATCAAAGTCTTCTCCACATGCTCCTCCCACCTGATCTCCGTTA  
 CCTTATACTATGGCTCCATTCTCTACAATACTCCCGGCCAAGTTCAGCTACTCCCTCAAG  
 AGGGACAAAATGGTTTCTACCTTTTATACTATGCTGTTCCCATGTTGAATCCCATGATCTA  
 CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATTCTTCAAGTCAGCATAA  
 (SEQ ID NO: 352)

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**AOLFR191 sequences:**

MTGGGNITEITYFILLGFSDFPRIKVLFTIFLVIYITSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS  
FIDVCYISSTVPKMLSNLLQEQTITFVGCIQYFIFSTMGLSESLMTAMAYDRYAAICNPLLYS  
SIMSPTLCVWMVLGAYMTGLTASLFQIGALLQLHFCGSNVIRHFFCDMPQLLILSCTDTFFVQV  
5 MTAILTMFFGIASALVIMISYGYIGISIMKITSAGSPKAFNTCASHLTAVSLFYTSGIFVYLRSSS  
GGSSSFDRFASVFYTVVIPMLNPLIYSLRNKEIKDALKRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTTCATCCTGCTGGGATTCTCAGATT  
TTCCCAGGATCATAAAAAGTGCTCTTCACTATATTCCTGGTGATCTACATTACATCTCTGGCC  
10 TGGAACTCTCCCTCATTGTTTAAATAAGGATGGATTCCCACCTCCATACACCCATGTATTT  
CTTCCTCAGTAACCTGTCTTCATAGATGTCTGCTATATCAGCTCCACAGTCCCCAAGATGC  
TCTCCAACCTCTTACAGGAACAGCAAATCATCTTTTGTGGTTGTATTATTACAGTACTTT  
ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT  
ATGCTGCCATTTGTAACCCCTGCTCTATTCATCCATCATGTACCCACCCTCTGTGTTTGG  
15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATTCCAAATTGGTGCTTTGCT  
TCAACTCCACTTCTGTGGGTCTAATGTCTCATCAGACATTCTTCTGTGACATGCCCAACTGT  
TAATCTTGTCTGTACTGACACTTTCTTTGTACAGGTCATGACTGCTATATTAACCATGTTC  
TTTGGGATAGCAAGTGCCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA  
TGAAGATCACTTCAGCTAAAGGCAGTCCAAAGGCATTCAACACCTGTGCTTCTCATCTAAC  
20 AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTTGAGGTCCAGCTCTGGAGGTT  
CTTCAAGCTTTGACAGATTTGCATCTGTTTCTACACTGTGGTCATTCCCATGTAAATCCC  
TTGATTTACAGTTTGAGGAACAAAGAAATTAAGATGCCTTAAAGAGGTTGCAAAAGAGA  
AAGTGCTGCTGA (SEQ ID NO: 354)

**AOLFR192 sequences:**

MENNTEVTEFILVGLTDDPELQIPLFIVFLFIYLITLVGNLGMIELILLDSCLHTPMYFFLSNLSLV  
DFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLLASMA YDRYAALCKPLHY  
TTTMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFCRSNVVEHFFCDAPPLLTLSCSDNYISEM  
VIFVVGFNDFLSILVILISYLFIFITIMKMRSEGRQKAFSTCASHLTAVSIFYGTGIFMYLRPNSS  
30 HFMGTDKMASVFYAIVIPMLNPLVYSLRNKEVKSAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTGGGGTTAACTGATGACCCAGAA  
CTGCAGATCCCCTCTTCATAGTCTTCTCTTTTCATCTACCTCATCACTCTGGTTGGGAACCT  
GGGGATGATTGAATTGATTCTACTGGACTCCTGTCTCCACACCCCCATGTACTTCTTCCTCA  
35 GTAACTCTCCCTGGTGGACTTTGGTTATTCCTCAGCTGTCACTCCCAAGGTGATGGTGGG  
GTTTCTCACAGGAGACAAATTCATATTATATAATGCTTGTGCCACACAATTCTTCTCTTTG  
TAGCCTTTATCACTGCAGAAAGTTTCTCCTGGCATCAATGGCCTATGACCGCTATGCAGC  
ATTGTGTAAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTTGCCTGGCC  
ATAGGCTCCTACATCTGTGGTTTCTGAATGCATCCATTCACTGGGAACACTTTCAGGC  
40 TCTCCTTCTGTAGATCCAATGTAGTTGAACACTTTTTCTGTGATGCTCCTCCTCTCTTGA  
CTCTCATGTTTACAGAACTACATCAGTGAGATGGTTATTTTTTTTGTGGTGGGATTCAATG  
ACCTCTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTTATATTATACCATCATGAAG  
ATGCGCTCACCTGAAGGACGCCAGAAGGCCTTTTCTACTTGTGCTTCCCACCTTACTGCAG  
TTTCCATCTTTTATGGGACAGGAATCTTTATGTACTTACGACCTAACTCCAGCCATTTCATG  
45 GGCACAGACAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG  
TCTACAGCCTGAGGAACAAAGAGGTTAAGAGTGCCTTTAAAAAGACTGTAGGGAAGGCAA  
AGGCCTCTATAGGATTCATATTTTAA (SEQ ID NO: 356)

**AOLFR193 sequences:**

MENKTEVTQFILLGLTNDSELQVPLFITFPFIYIITLVGNLGIIVLIFWDSCLHNP MYFFLSNLSLV  
DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLLASMA YDRYA AVCKPLHY  
TTTMTTTVCARLAIGSYLCGFLNASIHTGDTFSLSFCKSNVHHFFCDIPAVMVLSCSDRHISEL  
VLIYVVSFNIFIALLVILISYTFIFITILKMHSASVYQKPLSTCASHFI AVGIFYGTIIFMYLQPSSSH  
SMDTDKMAPVFYTMVIPMLNPLVYSLRNKEVKSAFKKVVEKAKLSVGWSV (SEQ ID NO:  
55 357)

ATGGAAAATAAGACAGAAGTAACACAATTCATTCTTCTAGGACTAACCAATGACTCAGAA  
 CTGCAGGTTCCCTCTTTATAACGTTCCCTTCATCTATATTATCACTCTGGTTGGAAACCT  
 GGGAATTATTGTATTGATATTCTGGGATTCTGTCTCCACAATCCCATGTACTTTTTTCTCA  
 5 GTAACCTTGTCTCTAGTGGACTTTTGCTACTCTTCAGCTGTCACTCCCATCGTCATGGCTGGA  
 TTCCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAATGTATATCTTTGT  
 AGCTTTTGCCACTGTGGAAAATTACCTCTTGGCCTCAATGGCCTATGACCGCTATGCAGCA  
 GTGTGCAAACCCCTACATTACACCACAACCATGACAACAACCTGTGTGTGCTCGTCTGGCCA  
 TAGGCTCCTACCTCTGTGGTTTCCCTGAATGCCTCCATCCACACTGGGGACACATTTAGTCTC  
 10 TCTTCTGTAAAGTCCAATGAAGTCCATCACTTTTTCTGTGATATTCCAGCAGTCATGGTTCT  
 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTCTTATTTATGTTGTGAGCTCAATATCT  
 TTATAGCTCTCCTGGTTATCTTGATATCCTACACATTCATTTTTATCACCATCCTAAAGATG  
 CACTCAGCTTCAGTATACCAGAAGCCTTTGTCCACCTGTGCCTCTCATTTTCATGTCAGTCGG  
 CATCTTCTATGGGACTATTATCTTCATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA  
 CAGACAAAATGGCACCTGTGTTCTATACAATGGTCATCCCCATGCTGAACCTCTGGTCTA  
 15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT  
 GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

**AOLFR194 sequences:**

20 MERQONQSCVVEFILLGFSNYPELQGQLFVAFLVIYLVTLIGNAIIIVIVSLDQSLHVPMYLFLNL  
 SVVDLSFSAVIMPEMLVVLSTEKTTISFGGCFAQMYFILLFGGAECFLLGAMAYDRFAAICHPL  
 NYQMIMNKGVMFKLIIFSWALGFMLGTVQTSWVSSFPFCGLNEINHISCETPAVLELACADTFL  
 FEIYAFTGTFLIILVPFLILLSYIRVLFALIKMPSTTGRQKAFSTCAAHLSVTIFYGTASMTYLQ  
 PKSGYSPETKKVMSLSYSLLTPLLNLIIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO:  
 359)

25 ATGGAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC  
 CTGAGCTCCAGGGGCAGCTCTTTGTGGCTTTCTGGTTATTTATCTGGTGACCCTGATAGG  
 AAATGCCATTATTATAGTCATCGTCTCCCTAGACCAGAGCCTCCACGTTCCCATGTACCTGT  
 30 TTCTCCTGAACTTATCTGTGGTGGACCTGAGTTTCAGTGCAGTTATTATGCCTGAAATGCT  
 GGTGGTCTCTCTACTGAAAAAACTACAATTTCTTTTGGGGGCTGTTTTGCACAGATGTAT  
 TTCATCCTTCTTTTGGTGGGGCTGAATGTTTTCTTCTGGGAGCAATGGCTTATGACCGATT  
 TGCTGCAATTTGCCATCCTCTCAACTACCAAATGATTATGAATAAAGGAGTTTTATGAAA  
 TTAATTATATTTTCATGGGCCTTAGGTTTTATGTTAGGTACTGTTCAAACATCATGGGTATC  
 TAGTTTTCCCTTTTGTGGCCTTAATGAAATAACCATATATCTTGTGAAACCCAGCAGTGT  
 35 TAGAACTTGCATGTGCAGACACGTTTTTGTGTTGATACTTGTCTTACATTGAGTTCTGTTTGGCATCCTG  
 ATTATTTTGGTTCCTTTCTTGTGATACTTGTCTTACATTGAGTTCTGTTTGGCATCCTG  
 AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCGCTCACCTCACAT  
 CTGTGACCCTATTCTATGGCACAGCCAGTATGACTTATTTACAACCCAAATCTGGCTACTC  
 ACCGGAAACCAAGAAAGTGATGTCTTACTCACTTCTGACACCACTGCTGAATCTG  
 40 CTTATCTACAGTTTGCAGAAATAGTGAGATGAAGAGGGCTTTGATGAAATTATGGCGAAGG  
 CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

**AOLFR195 sequences:**

45 MIVQLICTVCFILAVNTFHVRSSFDLKAADDMEINQTLVSEFLLLGLSGYPKIEIVYFALILVMY  
 LVILIGNGVLIASIFDSHFHTPMYFFLGNLSFLDICYTSSVPSLTVSLISKRNISFSGCAVQMFF  
 GFAMGSTECLLLGMMAFDTRYVAICNPLRYPIILSKVA YVLMASVSWLSGGINS AVQTLLAMRL  
 PFCGNIIINHFACEILAVLKLACADISLNIITMVISNMAFLVLPMLVIFFSYMFILY TILQMNSATG  
 RRKAFSTCSAHLTVVIIFYGTIFFMYAKPKSQDLIGEEKLQALDKLISLFYGVVTPMLNPILYSLR  
 NKDVKAAVKYLLNKKPIH (SEQ ID NO: 361)

50 ATGATTGTTTCAGTTAATTTGTACTGTTTGTCTTGGCAGTAAATACATTTTCATGTTAGATC  
 TTCTTTTGATTTCTGAAAGCAGATGACATGGGTGAGATTAACCAGACACTTGTGTCAGAA  
 TTTCTTCTTCTGGGTCTTTCTGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATTCT  
 AGTTATGTACCTAGTGATTCTAATTGGCAATGGTGTCTAATCATAGCCAGCATCTTTGATT  
 55 CTCATTTTCACACACCAATGTACTTCTTCTGGGCAACCTCTCTTCTGATATCTGCTAT  
 ACATCCTCCTCTGTTCCTCAACATTGGTGAGCTTAATCTCAAAGAAAAGAAACATTTCTCT



TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGCAATGGGGTCAACAGAATGTCTGCT  
TCTTGGCATGATGGCATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC  
ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTTCTGTGTCCTGGCTGTCCGGTGAATAA  
ATTCAGCTGTGCAAACATTACTTGCCATGAGACTGCCTTTCTGTGGGAATAATATTATCAA  
5 TCATTTTCGCATGTGAAATATTAGCTGTCTCAAGCTGGCCTGTGCTGATATATCCCTCAATA  
TTATCACCATGGTGATATCAAATATGGCCTTCCTGGTTCTTCCACTGATGGTCATTTTTTTC  
TCCTATATGTTTCATCCTCTACACCATCTTGCAAATGAATTCAGCCACAGGAAGACGCAAGG  
CATTTTCCACGTGCTCAGCTCACCTGACTGTGGTGATCATATTTTACGGTACCATCTTCTTT  
ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAAATTGCAAGCATTAGAC  
10 AAGCTCATTTCTCTGTTTATGGGGTAGTGACACCCATGCTGAATCCTATACTCTATAGCTT  
GAGAAATAAGGATGTAAAAGCTGCTGTAAAATATTGCTGAACAAAAAACCAATTCATA  
A (SEQ ID NO: 362)

**AOLFR196 sequences:**

15 MLESNYTMPTEFLFVGFTDYLPLRVTLFLVFLVYTLTMVGNILLIILVNINSSLQIPMYFSLNL  
SFLDISCSTAITPKMLANFLASRKSISPYGCALQMFFFAFADAECILILAAAMAYDRYAAICNPLL  
YTTLMSSRRVCVCFIVLAYFSGSTTSLVHVCLTFRLSFCGSNIVNHFFCDIPLLALSCTDTQINQL  
LLFALCSFIQTSTFVVFISYFCILITVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS  
YSLDTDKVVAVFYTVVFPMPNPIHSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ  
20 ID NO: 363)

ATGTTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTTGTTGGATTACAGATTATC  
TACCTCTCAGAGTCACACTGTTCTTGGTATTCTTCTGGTATATACATTAACATGGTCGGA  
AATATACTCTTAATAATTCTAGTTAATATTAATTCAAGCCTTCAAATTCCCATGTATTATTT  
25 TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTTCTACAGCAATCACTCCTAAAATGCTGG  
CAAACCTCTTGGCATCCAGGAAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTTT  
CTTCGCTTCTTTTGCTGATGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGACCGCTATG  
CAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGTCTGTGTCTGCTT  
CATTGTGTTGGCATATTTCAAGTGAAGTACAACATCACTGGTCCATGTGTGCCTCACATTC  
30 AGGCTGTCAATTTGTGGCTCCAATATCGTCAATCATTTTTTCTGTGATATCCCACCTCTTCT  
GGCTTTATCATGTACAGACACTCAGATCAACCAGCTTCTGCTCTTTGCTTTGTGCAGCTTCA  
TCCAGACCAGCACTTTTGTGGTAATATTTATTTCTTACTTCTGCATCCTCATCACTGTGTTG  
AGCATCAAGTCCTCAGGTGGCAGAAGCAAAACATTCTCCACTTGTGCTTCCCACCTCATAG  
CAGTCACCTTATTCTATGGAGCGCTCCTGTTTATGTACTTACAGCCCACCACCTATTCC  
35 CTAGACACTGATAAGGTGGTGGCAGTGTTTTATACTGTTGTATTTCCCATGTTTAATCCAA  
TAATTTATAGTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA  
TTGGATATTCAAATGAATGGTATTTAAATCGTTTAAGAATAGTCAATATCTAA (SEQ ID NO:  
364)

**AOLFR197 sequences:**

40 MCYLSQLCLSLGEHTLHMGMRHTNESNLGFIILLGFSYDYPQLQKVLFLVILILYLLTILGNNTI  
ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNSHALGS  
TECVLLALMSCDRYVAVCRPLHYTVLMHIHLCLMALASMAWLSGIATTLVQSTLTLLQLPFCGH  
RQVDHFICEVPVLIKLAFCVGTTFNEAELFVASILFLIVPVSFILVSSGYIAHAVLRIKSATRRQKAF  
45 GTCFSLTLTVTIFYGTIIFMYLQPAKSRSDQGKFSVSLFYTVVTRMLNPLIYTLRIKEVKGALKK  
VLAKALGVNIL (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG  
TGAGACATACCAATGAGAGCAACCTAGCAGGTTTCATCCTTTTAGGGTTTTCTGATTATCC  
50 TCAGTTACAGAAGGTTCTATTTGTGCTCATATTGATTCTGTATTTACTAACTATTTTGGGGA  
ATACCACCATCATTCTGGTTTCTCGTCTGGAACCCAAGCTTCATATGCCGATGTATTTCTTC  
CTTTCTCATCTCTCCTTCTGTACCGCTGCTTACCAGCAGTGTTATTCCCCAGCTCCTGGT  
AAACCTGTGGGAACCCATGAAAACATCGCCTATGGTGGCTGTTTGGTTTACCTTTACAAC  
TCCCATGCCCTGGGATCCACTGAGTGCCTCTTGGCTCTGATGTCCTGTGACCGCTATGT  
55 GGCTGTCTGCCGCTCTCCTTACACTGTCTTAATGCATATCCATCTCTGCATGGCCTTGG  
CATCTATGGCATGGCTCAGTGGAATAGCCACCACCCTGGTACAGTCCACCCTCACCCTGCA

5 GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTTCATCTGCGAGGTCCCTGTGCTCATC  
AAGCTGGCTTGTGTGGGCACACGTTTAACGAGGCTGAGCTTTTTGTGGCTAGTATCCTTT  
TCCTTATAGTGCCTGTCTCATTACCTGGTCTCCTCTGGCTACATTGCCACGCAGTGTTG  
AGGATTAAGTCAGCTACCAGGAGACAGAAAGCATTCTGGGACCTGCTTCTCCACCTGACA  
GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT  
CCAGGGACCAGGGCAAGTTTGTCTCTCTTCTACACTGTGGTAACCCGCATGCTTAACCC  
TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAA  
GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)

10 **AOLFR198 sequences:**

MENCTEVTKFILLGLTSVPELQIPLFILFTFIYLLTLCGNLGMMLLILMDSCLHTPMYFFLSNLSL  
VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFFFVALATVENYLLASMAYDRYAAVCKP  
LHYTTTMTASVGACLALGSYVCGFLNASFHIGGIFSLSFCKSNLVHHFFCDVPVAVMALSCSDKH  
TSEVILVFMSSFNIFVLLVIFISYLFIFITILKMHSAGHQKALSTCASHFTAVSVFYGTVIFIYLQ  
15 PSSSHSMDTDKMASVFYAMIIPMLNPVVYSLRNREVQNAFKKVLRRQKFL (SEQ ID NO: 367)

20 ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCCAGAAC  
TACAGATCCCCCTCTTTATCTTGTTCACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG  
GGGATGATGTTGCTGATCCTGATGGACTCTTGTCTCCACACCCCCATGTACTTTTTCTCAG  
TAACCTGTCTCTGGTGGACTTTGGATACTCCTCAGCTGTCACTCCCAAGGTCATGGCTGGG  
TTCCTTAGAGGAGACAAGGTCATCTCCTACAATGCATGTGCTGTTTCTCAGATGTTCTTCTTGT  
AGCCTTGCCACGGTGGAAAATTACTTGTGGCCTCAATGGCCTATGACCGCTATGCAGCA  
GTGTGCAAACCCCTACACTACACCACCACCATGACGGCCAGTGTAGGTGCCTGTCTGGCCC  
TAGGCTCATATGTCTGTGGCTTCCTAAATGCCTCATTCCACATTGGGGGCATATTCAGTCTC  
25 TCTTTCTGTAAATCCAATCTGGTACATCACTTTTTCTGTGATGTTCCAGCAGTCATGGCTCT  
GTCTTGCTCTGATAAACACACTAGTGAGGTGATTCTGGTTTTTATGTCAAGCTTTAATATCT  
TTTTTGTCTTCTAGTTATCTTTATCTCCTACTTGTTCATATTTCATACCATCTTGAAGATGC  
ATTGAGCTAAGGGACACCAAAAAGCATTGTCCACCTGTGCCTCTCACTTCACTGCAGTCTC  
CGTCTTCTATGGGACAGTAATCTTCATCTACTTGCAGCCAGCTCCAGCCACTCCATGGAC  
30 ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCCATGCTGAACCCCTGTGGTCT  
ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTTGAGAAGGCAAAAAT  
TTCTATAA (SEQ ID NO: 368)

**AOLFR199 sequences:**

35 MDTGNKTLQPQDFLLLGFPQSQTLLSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS  
NLSFLEIWYTAAVPAKALAILLGRSQTISFTSCLLQMYFVFSLGCTEYFLAAMAYDRCLAICY  
LHYGAIMSSLLSAQLALGSWVCGFVAIAVPTALISGLSFCGPRAINHHFFCDIAPWIALACTNTQA  
VELVAFVIAVVVILSSCLITFVSYYIISTILRIPSASGRSKAFSTCSSHLTVVLIWYGSTVFLHVR  
TSIKDALDLIAVHVLNTVTVPLNPFYTLRNKEVRETLKKWKWK (SEQ ID NO: 369)

40 ATGGACACAGGCAACAAAACCTCTGCCCCAGGACTTTCTCTTACTGGGCTTTCCTGGTTCTC  
AAACTCTTCAGCTCTCTCTCTTTATGCTTTTCTGGTGATGTACATCCTCACAGTTAGTGGT  
AATGTGGCTATCTTGATGTTGGTGAGCACCTCCCATCAGTTGCATACCCCCATGTACTTCTT  
TCTGAGCAACCTCTCCTTCTGGAGATTTGGTATACCACAGCAGCAGTGCCCCAAAGCACTG  
45 GCCATCCTACTGGGGAGAAGTCAGACCATATCATTTACAAGCTGTCTTTTGACAGATGTACT  
TTGTTTTCTCATTAGGCTGCACAGAGTACTTCTCCTGGCAGCCATGGCTTATGACCGCTGT  
CTTGCCATCTGCTATCCTTTACACTACGGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC  
TGGCCCTGGGCTCCTGGGTGTGTGGTTTCGTGGCCATTGCAAGTGCCACAGCCCTCATCAG  
TGGCCTGTCTTCTGTGGCCCCCGTGCCATCAACCACTTCTTCTGTGACATTGCACCCTGGA  
50 TTGCCCTGGCCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATTGCTGTTGT  
GGTTATCCTGAGTTCATGCCTCATCACCTTTGTCTCCTATGTGTACATCATCAGCACCATCC  
TCAGGATCCCCCTCTGCCAGTGGCCGGAGCAAAGCCTTCTCCACGTGCTCCTCGCATCTCAC  
CGTGGTGCTCATTTGGTATGGGTCCACAGTTTTCCTTCACGTCCGCACCTCTATCAAAGAT  
GCCTTGGATCTGATCAAAGCTGTCCACGTCTGAACACTGTGGTGACTCCAGTTTAAACC  
55 CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG  
GAAAATAA (SEQ ID NO: 370)

**AOLFR200 sequences:**

MTRKNYTSLTEFVLLGLADTLELQIILFLFFLVYITLTVLGNLGMILLIRIDSQ LHTPMYFFLANL  
SFVDVCNSTTITPKMLADLLSEKKTISFAGCFLOMYFFISLATTECILFGLMAYDRYAAICRPLL  
5 YSLIMSRTVYLKMAAGAFAGLLNFMVNTSHVSSLSFCDNSVIHHFFCDSPPLFKLSCSDTILKE  
SISSILAGVNIVGTLVLSSYSYVLFISFMSHSGEGRHRAFSTCASHLTAILFYATCIYTYLRPSS  
SYSLNQDKVASVFYTVVIPMLNPLIYSLRSKEVKKALANVISRKRRTSSFL (SEQ ID NO: 371)

ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGC  
10 TGGAGCTACAGATTATCCTCTTTTTGTTTTTCTTGTGATTATACACTTACAGTACTGGGA  
AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCCAGCTTCACACACCCATGTATTTCTT  
CCTGGCTAACCTGTCCTTTGTGGACGTTGTAACTCAACTACCATCACCCCAAAGATGCTG  
GCAGATTTATTATCAGAGAAGAAAACCATCTCTTTGCTGGCTGCTTCCTACAGATGTACT  
TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTAAATGGCCTATGACAGGTA  
15 TGCGGCCCATATGTCGCCCCGCTGCTTTACTCCTTGATCATGTCCAGGACCGTCTACCTAAAA  
ATGGCAGCCCGGGGCTTTTGTGTCAGGGTGTGCTGAACTTCATGGTCAACACAAGCCATGTCA  
GCAGCTTGTCATTCTGTGACTCCAATGTCATCCATCATTCTTCTGTGACAGTCCCCCACTT  
TTCAAGCTCTCTTGTTCTGACACAATCCTGAAAGAAAGCATAAGTTCTATTTTGGCTGGTG  
TGAATATTGTGGGGACTCTGCTTGTATCCTCTCCTCCTACTCCTACGTTCTCTTCTCCATT  
20 TTTTCTATGCATTCCGGGGAGGGGAGGCACAGAGCTTTCTCCACGTGTGCCTCTCACCTGA  
CAGCCATAATTCTGTCTATGCCACCTGCATCTATACTTACCTGAGACCTAGTTCCAGCTAC  
TCCCTGAATCAGGACAAAGTGGCTTCTGTGTTCTACACAGTGGTGATTCCCATGTTGAATC  
CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAGGCTTTAGCGAATGTAATTAGCA  
GGAAAAGGACCTCTTCCTTTCTGTGA (SEQ ID NO: 372)

25

**AOLFR201 sequences:**

MEWENHTILVEFFLKGLSGHPRELELFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL  
SFLDICYTTTTSIPSTLVSFLSERKTISLSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR  
YPIIMSKDAYVPMAAGSWIIGAVNSAVQSVFVQLPFCRNNINHTCEILAVMKLACADISDN  
30 EFIMLVATTLFILTPLLLIIVSYTLIIVSIFKISSSEGRSKASSTCSAHLTVVIIFYGTILFMYMKPKS  
KETLNSDDL DATDKIISMFGVMTMPMNPLIYSLRNKDVK EAVKHLNRRFFSK (SEQ ID NO:  
373)

ATGGAATGGGAAAACACACCACTTCTGGTGGAATTTTTTCTGAAGGGACTTTCTGGTCACC  
35 CAAGACTTGAGTTACTCTTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG  
AATGGTACTCTCATTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT  
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG  
TGAGCTTCCTTT CAGAAAGAAAGACCATTTCCTTTCTGGCTGTGCAGTGCAGATGTTCTT  
CGGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT  
40 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA  
TGGCAGCTGGGTCCTGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTGTTGTTGGT  
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTTACCTGTGAAATTCTGGCTGTC  
ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT  
TGTTTCATATTGACACCTTTGTTATTAATCATTGTCTCTTACACGTTAATCATTGTGAGCATC  
45 TTCAAAATTAGCTCTTCCGAGGGGAGAAGCAAAGCTTCCTCTACCTGTTTACGCCATCTGA  
CTGTGGTCATAATATTCTATGGGACCATCCTCTTCATGTACATGAAGCCCAAGTCTAAAGA  
GACACTTAATTTCGGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTG  
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCA  
GTAAAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

50

**AOLFR202 sequences:**

MEWENHTILVEFFLKGLSGHPRELELFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL  
SFLDICYTTTTSIPSTLVSFLSERKTISLSGCAVQMFLSLAMGTTECVLLGVMAFDRYVAICNPLR  
YPIIMSKDAYVPMAAGSWIIGAVNSAVQTVFVQLPFCRNNIINHTCEILAVMKLACADISGN  
55 EFILLVTTTLFLLTPLLLIIVSYTLIILSIFKISSSEGRSKPSSTCSARLTVVITFCGTIFL MYMKPKSQ

ETLNSDDLDATDKLIFFYRVMTMMNPLIYSLRNKDVKEAVKHLLRRKNFNK (SEQ ID NO: 375)

5 ATGGAATGGGAAAACACACCACTTCTGGTGGAATTTTTCTGAAGGGACTTTCTGGTCACC  
CAAGACTTGAGTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG  
AATGGTACTCTCATTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT  
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG  
TGAGCTTCCTTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCT  
10 CAGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCGTGATGGCCTTTGACCGCTAT  
GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA  
TGGCAGCTGGGTCCTGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTTTGTGGT  
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTTCTAGCTGTC  
ATGAAACTGGCCTGTGCTGACATCTCAGGCAATGAGTTCATCCTGCTTGTGACCACAACAT  
15 TGTTCCTATTGACACCTTTGTTATTAATTATTGTCTCTTACACGTTAATCATTTTGAGCATC  
TTCAAAATTAGCTCTTCGGAGGGGAGAAGCAAACCTTCTCTACCTGCTCAGCTCGTCTGA  
CTGTGGTGATAACATTCTGTGGGACCATCTTCCCTCATGTACATGAAGCCCAAGTCTCAAGA  
GACACTTAATTCAGATGACTTGGATGCCACTGACAACTTATATTATATTCTACAGGGTG  
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA  
GTAAACACCTACTGAGAAGAAAAAATTTTAACAAGTAA (SEQ ID NO: 376)

20

**AOLFR203 sequences:**

15 MKRQNQSCVVEFILLGFSNPELQVQLFGVFLVIYVVTLMGNAITVIISLNQSLHVPMYLFLLN  
LSVVEVSFAVITPEMLVVLSTEKTMISFVGCAQMYFILLFGGTECFLLGAMAYDRFAAICHPL  
NYPVIMNRGVFMKLVIFSWISGIMVATVQTTWVFSFPFCGPNEINHLFCETPPVLELVCADTFLF  
25 EIYAFTGTILVMPFLLILLSYIRVLFALKMPSTTGRQKAFSTCASHLTSVTLFYGTANMTYLQ  
PKSGYSPETKKLISLAYTLLTPLLNPLIYSLRNSEMKRTLKLRKRVILHTF (SEQ ID NO: 377)

30 ATGAAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCCTGGGCTTTTCTAACTTTC  
CTGAGCTCCAGGTGCAGCTCTTTGGGGTTTTCTAGTTATTTATGTGGTGACCCTGATGGG  
AAATGCCATCATTACAGTCATCATCTCCTTAAACCAGAGCCTCCACGTTCCCATGTACCTGT  
TCCTCCTGAACCTATCTGTGGTGGAGGTGAGTTTTCAGTGCAGTCATTACGCCTGAAATGCT  
GGTGGTGCTCTCTACTGAGAAAACCTATGATTTCTTTTGTGGGCTGTTTTGCACAGATGTAT  
TTCATCCTTCTTTTTGGTGGGACTGAATGTTTTCTCCTGGGAGCGATGGCTTATGACCGATT  
TGCTGCAATTTGCCATCCTCTGAACTACCCAGTGATTATGAACAGAGGGGTTTTTATGAAA  
35 TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGACCACTTGGGTAT  
TTAGTTTTCCATTTTGTGGCCCCAATGAAATTAATCATCTCTTCTGTGAGACTCCCCCGGTA  
CTAGAGCTTGTGTGTGCAGACACCTTCTTATTTGAAATCTATGCCTTCACAGGCACCATTTT  
GATTGTTATGGTTCCTTTCTTGTGATCCTCTTGTCTTACATTTCGAGTTCTGTTTGCCATCCT  
GAAGATGCCATCAACTACTGGGAGACAAAAGGCCCTTTCCACCTGTGCCTCTCACCTCACA  
40 TCTGTGACCCTGTTCTATGGCACAGCCAATATGACTTATTTACAACCCAAATCTGGCTACTC  
ACCCGAAACCAAGAACTGATCTCATTGGCTTACACGTTGCTTACCCCTCTGCTCAATCCG  
CTCATCTATAGCTTACGAAACAGTGAGATGAAGAGGACTTTGATAAACTATGGCGAAGA  
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

45 **AOLFR204 sequences:**

MEKKKNVTEFILGLTQNPIMEKVTFVVFLVLYMITLSGNLLIVVTITTSQALSSPMYFFLTHLSL  
IDTVYSSSSAPKLIVDSFQEKIISFNGCMAQAYAEHIFGATEIILLTVMACDCYVAICKPLNYTT  
IMSHSLCILLVAVAWVGFLHATIQILFTVWLPFCGPNVIGHFMCPLYLLKLVCIDHTLGLFV  
AVNSGFICLLNFLILVVSIVILRSLKNSLEGRCKALSTCISHIIVVVLFFVPCIFVYLRSVTTLPI  
50 DKAVAVFYTMVVPMLNPVVYTLRNAEVKSAIRKLWRKKVTSND (SEQ ID NO: 379)

ATGGAGAAGAAAAAGAATGTGACTGAATTCATTTTAATAGGTCTTACACAGAACCCCATATA  
ATGGAGAAAGTCACGTTTGTAGTATTTTGGTTCTTTACATGATAACACTTTCAGGCAACC  
TGCTCATTGTGGTTACCATTACCACCAGCCAGGCTCTGAGCTCCCCCATGTACTTCTTCCTG  
55 ACCCACCTTTCTTTGATAGACACAGTTTATTCTTCTTCTTACAGCTCCTAAGTTGATTGTGGA  
TTCCTTTCAAGAGAAGAAAATCATCTCCTTTAATGGGTGTATGGCTCAAGCCTATGCAGAA

CACATTTTGGTGCTACTGAGATCATCCTGCTGACAGTGATGGCCTGTGACTGCTATGTGG  
 CCATCTGCAAACCTCTGAACTACACAACCATTATGAGCCACAGCCTGTGCATTCTCCTGGT  
 GGCAGTGGCCTGGGTGGGAGGATTTCTTCATGCAACTATTCAGATTCTCTTTACAGTATGG  
 CTGCCCTTCTGTGGCCCAATGTCATAGGCCACTTCATGTGTGACTTGTACCCATTGTTAA  
 5 ACTTGTGTTGCATAGACACTCATACCCCTGGTCTCTTTGTTGCTGTGAACAGTGGGTTATCT  
 GCTTATTAAACTTCCTTATCTTGGTGGTATCCTATGTGATCATCTTGAGATCTTTAAAGAAC  
 AATAGCTTGGAGGGGAGGTGTAAAGCCCTCTCCACCTGTATTTCTCACATCATAGTAGTTG  
 TCTTATTCTTTGTGCCCTGTATATTTGTGTATCTGCGCTCAGTGACCACTCTGCCCATTTGAT  
 AAAGCTGTTGCTGTATTTTATACTATGGTGGTCCCAATGTTAAATCCCGTGGTCTACACAC  
 10 TCAGAAATGCTGAGGTAAAAAGTGCAATAAGGAAGCTTTGGAGAAAAAAGTGACTTCAG  
 ATAATGATTAA (SEQ ID NO: 380)

**AOLFR205 sequences:**

MESENRTVIREFILLGLTQSQDIQLLVFVLVLIFYFIILPGNFIIFTIKSDPGLTAPLYFFLGNLAFL  
 15 DASYSFTVAPRMLVDFLSAKKIISYRGCTQLFFLHFLGGEGLLLVVMAFDRIYIAICRPLHYPT  
 VMNPRTCYAMMLALWGGFVHSIIQVVLRLPFCGPNQLDNFFCDVPQVIKLACTDTFVVEL  
 LMVFNGLMTLLCFLGLLASVAVILCRIRGSSSEAKNKAMSTCITHIIVIFFMFGPGIFIYTRPFRA  
 FPADKVVSLFHTVIFPLNPVIYTLRNQEVKASMKKVFKNHIA (SEQ ID NO: 381)

20 ATGGAAAGCGAGAACAGAACAGTGATAAGAGAATTCATCCTCCTTGGTCTGACCCAGTCT  
 CAAGATATTCAGCTCCTGGTCTTTGTGCTAGTTTAAATATTCTACTTCATCATCCTCCCTGG  
 AAATTTTCTCATTATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCT  
 TTCTGGGCAACTTGGCCTTCTGATGCATCCTACTCCTTCACTGTGGCTCCCCGGATGTTG  
 GTGGACTTCTCTCTGCGAAGAAGATAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTT  
 25 TCTTGCACTTCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTA  
 CATCGCCATCTGCCGGCCTCTGCACTATCCTACTGTCATGAACCCTAGAACCTGCTATGCA  
 ATGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCTCATCCT  
 CCGCTTGCCTTTTTGTGGCCCAAACCAGCTGGACAACCTTCTTCTGTGATGTCCACAGGTC  
 ATCAAGCTGGCCTGCACCGACACATTTGTGGTGGAGCTTCTGATGGTCTTCAACAGTGGCC  
 30 TGATGACACTCCTGTGCTTTCTGGGGCTTCTGGCCTCCTATGCAGTCATTCTTTGTGCATA  
 CGAGGGTCTTCTTCTGAGGCAAAAAACAAGGCCATGTCCACGTGCATCACCCATATCATTG  
 TTATATTCTTCATGTTTGGACCTGGCATCTTCATCTACACGCGCCCTTCAGGGCTTTCCCA  
 GCTGACAAGGTGGTTTCTCTCTTCCACACAGTGATTTTCTTTGTTGAATCCTGTCAATTA  
 TACCCTTCGCAACCAGGAAGTGAAAGCTTCCATGAAAAAGGTGTTTAATAAGCACATAGC  
 35 CTGA (SEQ ID NO: 382)

**AOLFR206 sequences:**

MANRNNVTEFILLGLTENPKMQKIIFVVSVIYINAMIGNVLIVVTITASPSLRSPMYFFLAYLSFI  
 40 DACYSSVNTPKLITDSLYENKTILFNGCMTQVFGEHFFRGVEVILLTVMAYDHYVAICKPLHYT  
 TIMKQHVCSLLVGVSWSVGGFLHATIQILFICQLPFCGPNVIDHFMCDLYTLINLACTNTHLGLF  
 IAANSGFICLLNCLLLVSCVVILYSLKTHSLEARHEALSTCVSHITVVILSFIPCFVYMRPPATL  
 PIDKAVAVFYTMITSMLNPLIYTLRNAQMKNAIKRLCSRKAISSVK (SEQ ID NO: 383)

45 ATGGCGAATAGAAACAATGTGACAGAGTTTATTCTATTGGGGCTTACAGAGAATCCAAAA  
 ATGCAGAAAATCATATTTGTTGTGTTTCTGTCTATCTACATCAACGCCATGATAGGAAATG  
 TGCTCATTGTGGTCAACCATCACTGCCAGCCCATCACTGAGATCCCCCATGTACTTTTCTCTG  
 GCCTATCTCTCCTTTATTGATGCCTGCTATTCCTCTGTCAATACCCCTAAGCTGATCACAGA  
 TTCACTCTATGAAAAACAAGACTATCTTATTCAATGGATGTATGACTCAAGTCTTTGGAGAA  
 50 CATTTTTTCAGAGGTGTTGAGGTACCTACTTACTGTAATGGCCTATGACCACTATGTGG  
 CCATCTGCAAGCCCTTGCACTATACCACCATCATGAAGCAGCATGTTTGTAGCCTGCTAGT  
 GGGAGTGTGATGGGTAGGAGGCTTTCTTCATGCAACCATAACAGATCCTCTTCATCTGTCAA  
 TTACCTTTCTGTGGTCTAATGTCATAGATCACTTTATGTGTGATCTCTACACTTTGATCAA  
 TCTTGCTGCACTAATAACCCACACTCTAGGACTCTTCATTGCTGCCAACAGTGGGTTTCATAT  
 GCCTGTAAACTGTCTCTTGCTCCTGGTCTCCTGCGTGGTCATACTGTACTCTTAAAGACC  
 55 CACAGCTTAGAGGCAAGGCATGAAGCCCTCTCTACCTGTGTCTCCACATCACAGTTGTCA  
 TCTTATCCTTTATACCCTGCATATTTGTGTACATGAGACCTCCAGCTACTTTACCCATTGAT

AAAGCAGTTGCTGTATTCTACACTATGATAACTTCTATGTTAAACCCCTTAATCTACACCTT  
GAGGAATGCTCAAAATGAAAAATGCCATTAGGAAATTGTGTAGTAGGAAAGCTATTTCAAG  
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIIFDLSHLHTPMYFFLCN  
LSFLDVCYTSSSVPLILASFLAVKKKVSFSGCMVQMFISFAMGATECMILGTMALDRYVAICYP  
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFAMQLPFCANNVIKHFVCEILAILKLACADI  
SINVISM TGSNLIVLVIPLLVISISYIFIVATILRIPSTEGKHKAFSTCSAHLTVVIIFYGTIFFMYAKP  
10 ESKASVDSGNEDIIEALISLFYGVMTPLNPLIYSLRNKDVKA AVKNILCRKNFSDGK (SEQ ID  
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAATTTTTCCTGGTAGGGCTTTCTGCCACC  
CAAAGCTCCAGACAGTTTTCTTCGTTCTAATTTTGTGGATGTACCTGATGATCCTGCTTGGA  
15 AATGGAGTCTTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCATGTATTTCTT  
CCTCTGTAATCTTTCTTCCTCGACGTTTGCTACACAAGTTCCTCTGTCCCACTAATTCTTG  
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCTTCTCTGGGTGTATGGTGCAAATGTTTAT  
TTCTTTTGCCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCTAT  
GTGGCCATCTGCTACCCACTGAGATACCCTGTCATCATGAGCAAGGGTGCCTATGTGGCCA  
20 TGGCAGCTGGGTCCTGGGTCCTGGGCTGTGGACTCAGTAGTGACAGAGCTTTTGCAAT  
GCAGTTACCATTTCTGTGCTAATAATGTCATTAAACATTTTGTCTGTGAAATTTCTGGCTATCT  
TGAAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTATGACAGGGTGAATCTGAT  
TGTTCTGGTTATTCATTGTTAGTAATTTCCATCTCTTACATATTTATTGTTGCCACTATTCT  
GAGGATTCCTTCCACTGAAGGAAAAACATAAGGCCTTCTCCACCTGCTCAGCCACCTGACA  
25 GTGGTGATTATTTCTATGGAACCATCTTCTTCATGTACGCAAAGCCTGAGTCTAAAGCCT  
CTGTTGATTACAGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTTCTATGGAGTGAT  
GACTCCCATGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAAGGCTGCTGTC  
AAAAACATACTGTGTAGGAAAAACTTTTCTGATGGAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIIFAVCLLMYLITLLGNIFLISITILDSHLHTPMYFLSNL  
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP  
LRYPVIMNRRTCVQIAAGSWMTGCLTAMVEMMSVLPLSLCGNSINHTCEILAILKLVCVDTS  
LVQLIMLVISVLLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFGTALSMH  
35 LKPSAVDSQEIDKFMALVYAGQTPMLNPIIYSLRNKEVKVALKLLIRNHFNTAFISILK (SEQ  
ID NO: 387)

ATGTTCCCGGCAAATTGGACATCTGTAAAAGTATTTTCTTCCTGGGATTTTTTCACTACCC  
CAAAGTTCAGGTCATCATATTTGCGGTGTGCTTGCTGATGTACCTGATCACCTTGCTGGGC  
40 AACATTTTCTGATCTCCATCACCATTCTAGATTCCCACCTGCACACCCCTATGTACCTCTT  
CCTCAGCAATCTCTCCTTTCTGGACATCTGGTACTCCTCTTCTGCCCTCTCTCCAATGCTGG  
CAAACCTTTGTTTTCAGGGAGAAACACTATTTTATTCTCAGGGTGCGCCACTCAGATGTACCT  
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCCATGATGGCATATGACCGGTAT  
GTGGCCATCTGCAACCCCTGAGATACCCTGTCATCATGAATAGGAGAACCTGTGTGCAGA  
45 TTGCAGCTGGCTCCTGGATGACAGGCTGTCTCACTGCCATGGTGGAATGATGTCTGTGCT  
GCCACTGTCTCTGTGGTAATAGCATCATCAATCATTTCACTTGTGAAATTTCTGGCCATCT  
TGAAATGGTTTGTGTGGACACCTCCCTGGTGCAGTTAATCATGCTGGTGATCAGTGTACT  
TCTTCTCCCCATGCCAATGCTACTCATTTGTATCTCTTATGCATTTATCCTCGCCAGTATCC  
TGAGAATCAGCTCAGTGGAAGGTCGAAGTAAAGCCTTTTCAACGTGCACAGCCACCTGA  
50 TGGTGGTAGTTTGTCTATGGGACGGCTCTCTCCATGCACCTGAAGCCCTCCGCTGTAGA  
TTCACAGGAAATAGACAAATTTATGGCTTTGGTGTATGCCGGACAAACCCCATGTTGAAT  
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATTGCTGATTA  
GAAATCATTTTAATACTGCCTTCATTTCCATCCTCAAATAA (SEQ ID NO: 388)

**AOLFR209 sequences:**

MDKINQTFVREFILLGLSGYPKLEIIFLILVMYVVILIGNGVLIASILDSRLHMPMYFFLGNLS  
FLDICYTSSIPSTLVSLISKRNISFSGCAVQMFFGFAMGSTECFLLGMMAFDRYVAICNPLRY  
5 PIIMNKVVYVLLTSVSWLSGGINSTVQTSLAMRWPF CGNNIINHFLCEILAVLKLACSDISVNIV  
TLAVSNIAFLVPLLVIFFSYMFILY TILRTNSATGRHKAFSTCSAHLTVVIIFYGTIFFMYAKPKS  
QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:  
389)

10 ATGGACAAGATAAACCAGACATTTGTGAGAGAATTCATTCTTCTGGGACTCTCTGGTTACC  
CCAAACTTGAGATCATTTTCTTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC  
AATGGTGTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCCATGTAATTCTT  
CCTGGGCAACCTCTCTTCTGGATATCTGCTATACAACCTCCTCCATTCCCTCAACACTGG  
TGAGCTTAATCTCAAAGAAAAGAAACATTTCCCTTCTCTGGATGTGCAGTGCAGATGTTCTT  
15 TGGGTTTGCAATGGGGTCAACAGAATGTTTCCTCCTTGGCATGATGGCATTGTATCGTTAT  
GTGGCCATCTGTAACCCTCTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC  
TGACTTCTGTATCATGGCTTTCTGGTGGAATCAATTCAACTGTGCAAACATCACTTGCCAT  
GCGATGGCCTTTCTGTGGGAACAATATTATTAATCATTCTTATGCGAGATCTTAGCTGTCC  
TAAAATTAGCTTGTCTGATATATCTGCAATATTGTTACCCTAGCAGTGTCAAATATTGCT  
20 TTCTAGTTCTTCTCTGCTCGTGATTTTTTCTCCTATATGTTTCATCCTCTACACCATCTTG  
CGAACGAACCTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG  
TGGTGATCATATTTTATGGTACCATCTTCTTTATGTATGCAAAACCTAAGTCCCAGGACCTC  
CTTGGGAAAGACAACTTGCAAGCTACAGAGGGGCTTGTTCATGTTTTATGGGGTTGTGA  
CCCCCATGTTAAACCCATAATCTATAGCTTGAGAAATAAAGATGTAAAAGCTGCTATAAA  
25 ATATTGCTGAGCAGGAAAGCTATTAACAGTAA (SEQ ID NO: 390)

**AOLFR210 sequences:**

MMGRRNDTNVADFIL TGLSDSEEVQMALFMLFLLIYLITMLGNVGMILLIIRLDLQLHTPMYFFL  
THLSFIDLSYSTVVPKTLANLLTSNYISFTGCF AQMFCFVFLGTAECYLLSSMAYDRYAAICSP  
30 LH YTVIMPKRLCLALITGPYVIGFMDSFVNVVMSRLHFCD SNIIHHFFCDTSPILALSCTDTDN  
TEMLIFIAGSTLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGV TIFYGT MIFTYLPK  
RKSYSLGRDQVAPVFY TIVIPMLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)

35 ATGATGGGTTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC  
TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTTCTCCTCATATACCTAATTACTATGCT  
GGGGAATGTGGGGATGCTATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTAT  
TTTTTCCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAAC  
CTTAGCGAACTTACTGACTTCCAATAATTTCTTACGCGGCTGCTTTGCCAGATGTTCT  
40 GTTTTGTCTTCTTGGGTACTGCTGAATGTTATCTTCTCCTCAATGGCCTATGATCGCTAT  
GCAGCGATCTGCAGTCTCTACACTACACAGTTATTATGCCCAAAGGCTCTGCCTCGCTC  
TCATCACTGGGCCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC  
AGATTGCATTTCTGTGACTCAAACATAATTCATCACTTTTTCTGTGACACTTCCCCAATTTT  
AGCTCTGTCTGCTGACTGACACAGACAACACTGAAATGCTGATATTCATTATCGCTGGTTC  
ACCCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCT  
45 GAAAATTAATTCACCTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCGTCTCTCATCTCTTG  
GGAGTCACCATCTTCTATGGAAGTATGATTTTACTTACTTAAAGCCAAGAAAGTCTTATT  
CCTTGGGAAGAGATCAAGTGGCTCCTGTGTTTTATACTATTGTGATTCCCATGCTGAATCC  
ACTCATTTATAGTCTTAGAAACAGAGAAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG  
AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)

50

**AOLFR211 sequences:**

MMGRRNNTNVADFILMGLTLSEEIQMALFMLFLLIYLITMLGNVGMILLIIRLDLQLHTPMYFFL  
THLSFIDLSYSTVVPKTLANLLTSNYISFTGCF AQMFFAFLGTAECYLLSSMAH DRYAAICSP  
LHYTVIMSKRLCLALITGPYVIGFIDSFVNVVMSRLHFYDSNVIHHFFCDTSPILALSCTDTYNT  
55 EILIFIIVGSTLMVSLFTISASYVFILFTILKINSTSGKQKAFSTCVSHLLGV TIFYSTLIFTYLPKPRK  
SYSLGRDQVASVFY TIVIPVLNPLIYSLRNKEVKNAVIRVMQRRQDSR (SEQ ID NO: 393)

ATGATGGGTAGAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT  
 CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG  
 GGGAAATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATT  
 5 TTTTCCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTACACCTAAAACC  
 TTAGCGAACTTACTGACTTCCAATAATTTTCCTTTACGGGCTGCTTTGCCAGATGTTCTT  
 TTTTGCTTCTTGGGTACTGCTGAATGTTACCTTCTCTCCTCAATGGCCCATGATCGCTATG  
 CAGCGATCTGCAGTCCTCTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT  
 CATCACTGGGCCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA  
 10 GATTGCATTTCTACGACTCAAACGTAATTCATCACTTTTCTGTGACACTTCCCAATTTTA  
 GCTCTGTCTGCCTGACTGATACATAACAACACCGAAATCCTGATATTCATTATTGTTGGTTCCAC  
 CCTGATGGTGTCCCTTTTCACAATATCTGCATCCTATGTGTTCACTTCTCTTTACCATCCTGA  
 AAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCGTCTCTCATCTCTTGGG  
 AGTCACCATCTTTTATAGCACTCTGATTTTACTTATTTAAAACCAAGAAAGTCTTATTCCT  
 15 TGGGAAGAGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCGTGCTGAATCCACT  
 CATTTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTCATCAGAGTCATGCAGAGAAG  
 ACAGGACTCCAGGTAA (SEQ ID NO: 394)

**AOLFR212 sequences:**

20 MAGNNFTEVTVFILSGFANHPELQVSLFLMFLFIYLFVTLGNLGLITLIRMDSQLHTPMYFFLSN  
 LAFIDIFYSSTVTPKALVNFQSNRRSISFVGCFFVQMYFFVGLVCCCECFLGSMAYNRYIAICNPL  
 LYSVMSQKVS NWLGVMPIYVIGFTSSLISVWVISSLAFCDSINHHFCDTTALLALSCVDTFGT  
 EMVSFVLGFTLLSLLIITVTYIIISAILRIQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLPD  
 NTSSLTQAQVASVFYTIVIPMLNPLIYSLRNKDVKNALLRVIHRKLFP (SEQ ID NO: 395)

25 ATGGCTGGCAACAATTTCACTGAGGTTACCGTCTTCATCCTCTCTGGATTGCAAATCACC  
 CTGAATTACAAGTCAGTCTTTTCTTGATGTTTCTCTTCATTTATCTATTCACTGTTTTGGGA  
 AACCTGGGACTGATCACGTTAATCAGAATGGATTCTCAGCTTCACACCCCTATGTACTTTT  
 TCCTGAGCAATTTAGCATTTATTGACATATTTTACTCCTCTACTGTAACACCTAAGGCATTG  
 30 GTGAATTTCCAATCCAATCGGAGATCCATCTCCTTTGTTGGCTGCTTTGTTCAAATGTACTT  
 TTTTGTGGATTGGTGTGTTGTGAGTGTTTCTTCTGGGATCAATGGCCTACAATCGCTACA  
 TAGCAATCTGCAATCCCTTACTGTATTGAGTAGTCATGTCCCAAAAAGTGTCCTCACTGGCT  
 GGGAGTAATGCCATATGTGATAGGCTTCACAAGCTCGCTGATATCTGTCTGGGTGATAAGC  
 AGTTTGGCGTTCTGTGATTCCAGCATCAATCATTTTTTTTTGTGACACCACAGCTCTTTTAGC  
 35 ACTCTCCTGTGTAGATACATTGCGCACAGAAATGGTGAGCTTTGTCTTAGCTGGATTCACT  
 CTTCTTAGCTCTCTCCTTATCATCACAGTCACTTATATCATCATCATCTCAGCCATCCTGAG  
 GATCCAGTCAGCAGCAGGCAGGCAGAAGGCCTTCTCCACCTGCGCATCCCACTCATGGCT  
 GTAACATCTTTTATGGGTCTCTGATTTTACCTATTGCAACCTGATAACACATCATCGCT  
 GACCCAGGCGCAGGTGGCATCTGTATTCTATACGATTGTGATTCCCATGCTGAATCCACTC  
 40 ATCCAGTCTGAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAA  
 CTTTTCCATGA (SEQ ID NO: 396)

**AOLFR213 sequences:**

45 MNSLGKLVSMILSAHVFCYSKFNCFGCTHSIPALGADPPGGMGLGNESSLMDFILLGFS DHPRL  
 EAVLFVFFVLFYLLTLVGNFTIIISYLDPLHTPMYFFLSNLSLLDICFTTSLAPQTLVNLQRPKK  
 TITYGGCVAQLYISLALGSTECILLADMALDRYIAVCKPLHYVVMNPRLCQQLASISWLSGLA  
 SSLIHATFTLQLPLCGNHRLDHFICEVPALLKLACVDTTVNELVLFVSVLFFVIPPALISISYGF  
 IQAVLRIKSVEARHKAFTSCSSHLTVVIIFYGTIIYVYLQPSDSYAQDQGKFISLFYTMVPTLNP  
 IYTLRNKDMKEALRKLLSGKL (SEQ ID NO: 397)

50 ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTCTAA  
 ATTTAATTGTTTTGGATGTACCCATTCCATTCCTGCCTTAGGTGCGGATCCCCCTGGAGGG  
 ATGGGATTGGGCAATGAGAGTTCCCTAATGGATTTCATCCTTCTAGGCTTCTCAGACCACC  
 CTCGCTGGAGGCTGTTCTCTTTGTATTTGTCCTTTTCTTCTACCTCCTGACCTTGTGGGA  
 55 AACTTCACCATAATCATCATCTCATATCTGGATCCCCCTCTTCATACCCCAATGTACTTTTT  
 TCTCAGCAACCTCTCTTTACTGGACATCTGCTTCACTACTAGCCTTGCTCCTCAGACCTTAG



TTAACTTGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT  
 TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTTGGCTGACATGGCCTTGGATCGGTAC  
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTTGCCAACAGC  
 TGGCATCTATCTCCTGGCTCAGTGGTTTGGCTAGTTCCTAATCCATGCAACTTTTACCTTG  
 5 CAATTGCCTCTCTGTGGCAACCATAGGCTGGACCATTTTATTTGCGAAGTACCAGCTCTTCT  
 CAAGTTGGCTTGTGTGGACACCACTGTCAATGAATTGGTGCTTTTTTGTGTAGTGTCTGT  
 TTGTTGTCAATCCACCAGCACTCATCTCCATCTCCTATGGCTTCATAACTCAAGCTGTGCTG  
 AGGATCAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGCTCCTCCACCTTACAG  
 TGGTGATTATATTCTATGGCACCATAATCTACGTGTACCTGCAACCTAGTGACAGCTATGC  
 10 CCAGGACCAAGGGAAGTTTATCTCCCTCTTCTACACCATGGTGACCCCCACTTTAAATCCT  
 ATCATCTATACTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAACTTCTCTCGGGA  
 AAATTGTGA (SEQ ID NO: 398)

**AOLFR214 sequences:**

15 MDKSNSSVSEFVLLGLCSSQKLQLFYFCFFSVLYTVIVLGNLLIILTVTSDTSLHSPMYFLLGN  
 LSFVDICQASFTPCKMIADFLSAHETISFSGCIAQIFFIHLFTGGEMVLLVSMAYDRYVAICKPLY  
 YVIMSRRCTVLVMISWAVSLVHTLSQLSFTVNLPCGPNVVDSSFFCDLPRVTKLACLDSEYIE  
 ILIVVNSGILSLSTFSLVSSYIIILVTWVKSSAAMAKAFSTLASHIAVVILFFGPCIFYVWPFTIS  
 PLDKFLAIFYTVFTPVLNPIIYTLNRNMDKAAVRKIVNHYLRPRRISEMSLVVRTSFH (SEQ ID  
 20 NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTAAGTGTGGGACTCTGTAGTTCTC  
 AAAAAGTCCAGCTTTTCTATTTTTGTTTCTCTCTGTGTGTATACAGTCATTGTGCTGGGA  
 AATCTTCTCATTATCCTCACAGTGACTTCTGATACCAGCCTGCACTCCCCTATGTACTTTCT  
 25 CTTGGGAAACCTTTCCTTTGTTGACATTTGTGAGGCTTCTTTTGCTACCCCTAAAATGATTG  
 CAGATTTTCTGAGTGACACGAGACCATATCTTTCAGTGGCTGCATAGCCCAAATTTTCTT  
 ATTCACCTTTTTACTGGAGGGGAGATGGTGCTACTTGTTCGATGGCCTATGACAGGTATG  
 TAGCCATATGCAAACCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACTGTCTT  
 GGTAATGATCTCCTGGGCTGTGAGCTTGGTGACACATTAAGCCAGTTATCATTTACTGTG  
 30 AACCTGCCTTTTTGTGGACCTAATGTAGTAGACAGCTTTTTTTGTGATCTTCTCGAGTCAC  
 CAAACTTGCTGCCTGGACTCTTACATCATTGAAATACTAATTGTGGTCAATAGTGGAATT  
 CTTTCCCTAAGCACTTCTCTCTCTTGGTCAGCTCCTACATCATTATTCTTGTACAGTTTG  
 GCTCAAGTCTTCAGCTGCAATGGCAAAGGCATTTTCTACGCTGGCTTCCCATTTGACGTA  
 GTAATATTATTCTTTGGACCTTGCATCTTCTATCTATGTGTGGCCCTTACCATCTCTCTTT  
 35 GGATAAATTTCTTGCCATATTTTACACTGTTTTTACCCCCGTCCTAAACCCCATTTATTA  
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAGGAAAATTGTGAACCATTAACCTGAGGC  
 CAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCTTTTCAATTA (SEQ ID NO:  
 400)

**AOLFR215 sequences:**

40 MAHTNESMVSEFVLLGLSNSWGLQLFFFAIFSIVYVTSVLGNVLIIVISFDSHLNMPMYFLLSNL  
 SFIDICQSNFATPKMLVDFFIERKTISFEGCMAQIFVLHSFVGSEMMLLVAMAYDRFIAICKPLH  
 YSTIMNRRLCVIFVSISWAVGVLHVSHLAFTVDLPFCGPNVVDSSFFCDLPLVIELACMDTYEM  
 EIMTLTNSGLISLSCFLALISYTIILIGVRCRSSGSSKALSTLTAHITVVILFFGPCIFYWPFPSRL  
 45 PVDKFLSVFYTVCTPLNPIIYSLRNEDVKAAMWKLNRHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT  
 GGGGACTTCAACTTTTCTTTTCGCCATCTTCTCTATAGTCTATGTGACATCAGTGCTAGGC  
 AATGCTTAATTATTGTCAATTATTCTTTTACTCCCATTTGAACTCTCCTATGTACTTCTTG  
 50 CTCAGTAATCTTTCTTTTCAATTGATATCTGTGAGTCTAACTTTGCCACCCCCAAGATGCTTGT  
 AGACTTTTTTATTGAGCGCAAGACTATCTCCTTTGAGGGTTGCATGGCCAGATATTCTGTT  
 CTTACAGTTTTTGTGGGAGTGAGATGATGTTGCTTGTAGCTATGGCATATGACAGATTTA  
 TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTCTGTGTAATTTT  
 TGTGTCTATTTCTGGGCGGTGGGCGTTCTTCAATTCTGTGAGCCACTTGGCTTTTACAGTGG  
 55 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTTTGTGACCTTCCCTTGGTGATA  
 GAGCTGGCTTGCATGGATACATATGAAATGGAAATTATGACCCTAACGAACAGTGGCCTG

ATATCATTGAGCTGTTTCCTGGCTTTAATTATTTCTACACCATCATTTTGATCGGTGTCCG  
 ATGCAGGTCCTCCAGTGGGTCATCTAAGGCTCTTTCTACATTAAGTCCCCACATCACAGTG  
 GTCATTCTTTTCTTCGGGCCTTGCAATTTATTTCTATATATGGCCTTTTAGCAGACTTCCTGT  
 5 GGACAAATTTCTTTCTGTGTTCTACACTGTTTGTACTCCCTTGTGTAACCCCATCATCTACT  
 CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAAC  
 CCTGGAAAACTAG (SEQ ID NO: 402)

**AOLFR216 sequences:**

MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNLIVITVIVDPHLHSPMYFLL  
 10 TNLSIIDMSLASFATPKMITDYLTHGKTISFDGCLTQIFFLHLFTGTEILLMAMSFDRYIAICKPL  
 HYASVISPVQVCVALVVASWIMGVMHMSMQVIFALTLPCGPYEVDSPFCDLPVVFQLACVDY  
 VLGLFMISTSGIILSCFIVLFNSYVIVLVTVKHHSSRGSSKALSTCTAHFIVVFLFPGPCIFIYMW  
 PLSSFLTDKILSVFYTIPTPLNPIIYTLRNQEVKIAMRKLKNRFLNFKAMPS (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTTGTTTTGCTGGGGCTCTCTAATTCCT  
 GGGAACTACAGATGTTTTCTTTATGGTGTTCATTGCTTTATGTGGCAACAATGGTGGG  
 TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCTCACCTACACTCTCCTATGTATTTCC  
 TGCTTACCAATCTTTCAATCATTGATATGTCTCTTGCTTCTTCGCCACCCCAAAGATGATT  
 ACAGATTACCTAACAGGTCACAAAACCATCTCTTTGATGGCTGCCTTACCCAGATATTCT  
 20 TTCTCCACCTTTTCACTGGAAGTGAAGATCATCTTACTCATGGCCATGTCCTTTGATAGGTAT  
 ATTGCAATATGCAAGCCCCTGCACTATGCTTCTGTCTATTAGTCCCCAGGTGTGTGTGCTCT  
 CGTGGTGGCTTCTCTGGATTATGGGAGTTATGCATTCAATGAGTCAGGTCATATTTGCCCTC  
 ACGTTACCATTCTGTGGTCCCTATGAGGTAGACAGCTTTTCTGTGACCTTCCTGTGGTGTT  
 CCAGTTGGCTTGTGTGGATACTTATGTTCTGGGCCTCTTTATGATCTCAACAAGTGGCATA  
 25 ATTGCGTTGTCCTGTTTTATTGTTTTATTAAATTCATATGTTATTGTCCTGGTTACTGTGAA  
 GCATCATTCTTCCAGAGGATCATCTAAGGCCCTTTCTACTTGTACAGCTCATTTTATTGTTG  
 TCTTCTTGTCTTTGGGCCATGCATCTTCATCTACATGTGGCCACTAAGCAGCTTTCTCACA  
 GACAAGATTCTGTCTGTGTTTTATACCATCTTACTCCCACTCTGAACCAATAATCTATAC  
 TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAACTGAAAAATAGGTTTCTAAATTT  
 30 TAATAAGGCAATGCCTTCATAG (SEQ ID NO: 404)

**AOLFR217 sequences:**

MLESFQKSEQMAWSNQSAVTEFILRGLSSSLELQIFYFLFFSIVYAATVLGNLLIVVTIASEPHLH  
 SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAISFEFCMTQMFFLHLLGGAEIVLLISMSFD  
 35 RYVAICKPLHYLTIMSRMCVGLVILSWIVGIFHALSQLAFTVNLPCGPNEVDSPFCDLPLVIK  
 LACVDYIILGVFMISTSGMIALVCFILLVISYTHLVTVRQRSSGGSSKALSTCSAHFTVVTLFPGP  
 CTFIYVWPFTNFPIDKVLVSVFYTIYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRKTDHTP  
 (SEQ ID NO: 405)

40 ATGCTAGAGTCCTTCCAGAAATCAGAGCAAATGGCCTGGAGCAATCAGTCTGCGGTAACC  
 GAATTCATACTACGGGGTCTGTCCAGTTCTTTAGAACTCCAGATTTTCTACTTCCTGTTTTT  
 CTCCATAGTCTATGCAGCCACTGTGCTGGGGAACCTTCTTATTGTGGTCACCATTCATCA  
 GAGCCACACCTTCATTCCCCCTACGTACTTTCTGCTGGGCAATCTCTCCTTCATTGACATGTC  
 CCTGGCCTCATTGTCACCCCAAAATGATTGCAGACTTCCTTAGAGAACACAAAGCCATC  
 45 TCTTTTGAAGGCTGCATGACCCAGATGTTCTTCTACATCTCTTAGGGGGTGCTGAGATTG  
 TACTGCTGATCTCCATGTCCTTTGATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA  
 ACAATCATGAGCCGAAGAATGTGTGTTGGGCTTGTGATACTTTCTGATTGTGCGGCATCT  
 TCCATGCTCTGAGTCAGTTAGCATTTACAGTGAATCTGCCCTTCTGTGGACCCAATGAAGT  
 AGACAGTTTCTTTTGTGACCTCCCTTTGGTGATTAAACTTGCTTGTGTCGACACATATATTC  
 50 TGGGGGTGTTTCATGATCTCAACCAGTGGCATGATTGCCCTGGTGTGCTTCATCCTCTTGGT  
 GATCTCTTACACTATCATCCTGGTCACCGTTTCGGCAGCGTTCCTCTGGTGGATCCTCCAAA  
 GCCCTCTCCACGTGCAGTGCCCACTTTACTGTTGTGACCTTTTCTTTGGCCCATGCACTTT  
 CATTTATGTGTGGCCTTTCACAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA  
 TATACACTCCCCTCTTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATTC  
 55 CATGAGGAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA  
 (SEQ ID NO: 406)

**AOLFR218 sequences:**

METANYTKVTEFVLTGLSQTREVQLVLFVIFLSFYLFILPGNLIICTIRLDPHLTSPMYFLLANLA  
LLDIWYSSITAPKMLIDFFVERKIISFGGCIQLFFLHFVGASEMFLIVMAYDRYAAICRPLHYA  
5 TIMNRRLCCILVALSWMGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM  
ICSSGLISVVCFIALLSYAFLLALLKKHSGSDENTNRAMSTCYSHITIVLMFGPSIYIYARPD  
SFSLDKVVSVFHTVIFPLNPIIYTLRNKEVKAAMRKVVTKYLCEEK (SEQ ID NO: 407)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC  
10 GGGAGGTCCAAGTATGCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA  
AATATCCTTATCATTTGCACCATCAGGCTAGACCCTCATCTGACTTCTCCTATGTATTTCT  
GTTGGCTAATCTGGCCCTCCTTGATATTTGGTACTCTTCCATTACAGCCCCTAAATGCTCA  
TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTGGTGGATGCATTGCACAGCTCTTCTT  
CTTACACTTTGTTGGGGCTTCGGAGATGTTCTTGCTCATAGTGATGGCCTATGACCGCTAT  
15 GCTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCGACGTCTCTGCTGTATCCT  
GGTGGCTCTCTCCTGGATGGGGGGCTTCATTCTATAATACAGGTGGCTCTCATTGTT  
CGACTTCCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTG  
TCCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTAGTGATGATCTGTAGTAGTGGTCT  
GATCTCTGTGGTGTGTTTCATTGCTCTGTTAATGTCCTATGCCTTCTTCTGGCCTTGCTCA  
20 AGAAACATTGAGGCTCAGATGAGAATACCAACAGGCCATGTCCACCTGCTATTTCCCAT  
TACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCAT  
TTTCCCTAGATAAAGTGGTGTCTGTGTTTCTACTGTAATATTCCCTTACTTAATCCCAT  
ATTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGGTGGTCACCAAATAT  
ATTTTGTGTGAAGAGAAGTGA (SEQ ID NO: 408).

**AOLFR219 sequences:**

MLTSLTDLCSPIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSSRELQPFLFLTFSLLYLAILLGNF  
LIILTVTSDSRLHTPMYFLLANLSFIDVCVASFATPKMIADFLVERKTISFDACLAQIFFVHLFTGS  
EMVLLVSMAYDRYVAICKPLHYMTVMSRRVCVVLVLISWVFGFIHTTSQLAFTVNLFPFCGPN  
30 KVDSFFCDLPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVSYSYTVILVTVNRNSSASMAKAR  
STLTAHITVTVLFFGPCIFIYVWPFSYSVDKVLAVFYTIFTLILNPVIYTLRNKEVKAAMSKLKS  
RYLKPSQVSVIRNVLFLETK (SEQ ID NO: 409).

ATGCTCACTTCATTAAGTATGATCTCTGTTTCTCTCCTATTACAGGTAGCTGAAATTAAGTCCCT  
35 TCCAAAATCGATGAATGAGACAAATCATTCTCGGGTGACAGAATTTGTGTTGCTGGGACTG  
TCTAGTTCAAGGGAGCTCCAACCTTTCTTGTTTCTTACATTTTCACTACTTTATCTAGCAAT  
TCTGTTGGGCAACTTTCTCATCATCCTCACTGTGACCTCAGATTCCCGCCTTCACACCCCCA  
TGTACTTTCTGCTTGCAAACCTGTCATTTATAGACGTATGTGTTGCCTCTTTTGCTACCCCT  
AAAATGATTGCAGACTTTCTGGTTGAGCGCAAGACTATTTCTTTTGATGCCTGCCTGGCCC  
40 AGATTTTCTTTGTTTCATCTCTTCACTGGCAGTGAAATGGTGCTCCTAGTTTCCATGGCCTAT  
GACCGTTATGTTGCTATATGCAAACCTCTCCACTACATGACAGTCATGAGCCGTCGTGTAT  
GTGTTGTGCTCGTCTCATTTTCATGGTTTGTGGGCTTCATCCATACTACCAGCCAGTTGGCA  
TTCAGTGTTAATCTGCCATTTGTGGTCTTAATAAGGTAGACAGTTTTTTCTGTGACCTTCC  
TCTAGTGACCAAGTTAGCCTGCATAGACACTTATGTTGTCAGCTTACTAATAGTTGCAGAT  
45 AGTGGCTTTCTTTCTCTGAGTTCCTTTCTCCTCTTGTTGTCTCCTACACTGTAATACTTGT  
ACAGTTAGGAATCGCTCCTCTGCAAGCATGGCGAAGGCCCGCTCCACATTGACTGCTCACA  
TCACTGTGGTCACTTTATTCTTTGGACCATGCATTTTCATCTATGTGTGGCCCTTCAGCAGT  
TACTCAGTTGACAAAGTCCTTGCTGTATTCTACACCATCTTCACGCTTATTTTAAACCCTGT  
AATCTACACGCTAAGAAACAAAGAAGTGAAGGCAGCTATGTCAAACTGAAGAGTCGGTA  
50 TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCTAGAAACAAAGTAA  
(SEQ ID NO: 410).

**AOLFR220 sequences:**

MKQYSVGNQHSNYRSLFPFLCSQMTQLTASGNQTMVTEFLFSMPHAHRGGLLFFIPLLLIYG  
55 FILTGNLIMFIVIQVGMALHTPLYFFISVLSFLEICYTTTTIPKMLSCLISEQKSISVAGCLLQMYFF  
HSLGITESCULTAMAIDRYAICNPLRYPTIMIPKLCIQLTVGSCFCGFLVLPEIAWISTLPFCGS

NQIHQIFCDFTPVLSLACTDTFLVVIVDAIHAAEIVASFLVIALSYIRIIHILGMHSAEGHHKAFST  
CAAHLAVFLFFGSAVMYLRFSATYSVFWDTAIAVTFVILAPFFNPIIYSLKNKDMKEAIGRLF  
HYQKRAGWAGK (SEQ ID NO: 411).

5 ATGAAGCAATATTCAGTGGGTAATCAACATTCCAATTATAGGAGTCTCTTGTTCCTTTTCT  
GTGTTACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAATGGTGACTGAGTTCCT  
CTTCTCTATGTTCCCGCATGCGCACAGAGGTGGCCTCTTATTCTTTATTCCCTTGCTTCTCA  
TCTACGGATTTATCCTAACTGGAAACCTAATAATGTTCAATTGTCATCCAGGTGGGCATGGC  
CCTGCACACCCCTTTGTATTTCTTTATCAGTGTCTCTCCTTCCTGGAGATCTGCTATACCA  
10 CAACCACCATCCCCAAGATGCTGTCTGCCTAATCAGTGAGCAGAAGAGCATTTCCTGGC  
TGGCTGCCTCCTGCAGATGTACTTTTTCCACTCACTTGGTATCACAGAAAGCTGTGTCCTG  
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAACCATCA  
TGATTCCAAACCTTTGTATCCAGCTGACAGTTGGATCCTGCTTTTGTGGCTTCCTCCTTGTG  
CTTCTGAGATTGCATGGATTTCCACCTTGCTTTCTGTGGCTCCAACCAGATCCACCAGAT  
15 ATTCGTGATTTACACCTGTGCTGAGCTTGGCCTGCACAGATACATTCCTAGTGGTCATT  
GTGGATGCCATCCATGCAGCGGAAATTGTAGCCTCCTTCCTGGTCATTGCTCTATCCTACA  
TCCGGATTATTATAGTGATTCTGGGAATGCACTCAGCTGAAGGTCATCACAAGGCCTTTTC  
CACCTGTGCTGCTCACCTTGCTGTGTTCTTGCTATTTTTTGGCAGTGTGGCTGTCATGTATT  
TGAGATTCTCAGCCACCTACTCAGTGTGTTGGGACACAGCAATTGCTGTCACTTTTGTATC  
20 CTTGCTCCCTTTTTCAACCCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA  
TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGGAAATAG (SEQ ID NO:  
412).

**AOLFR221 sequences:**

25 MRNLSGGHVEFVLVGFPPTPPLQLLFVLFFAIYLLTLENALIVFTIWLAPSLHRPMYFFLGH  
LSFLELWYINVTIPRLAAFLTQDGRVSYVGCMTQLYFFIALACTECVLLAVMAYDRYLAICGP  
LLYPSLMPSSLATRLAAASWGSFGFSSMMKLLFISQLSYCGPNIIHFFCDISPLNLTCSDEKA  
ELVDLLALVMILLPLLAVSSYTAIIAAILRIPTSRGRHKAFSTCAAHLAVVVIYSSLTFTYAR  
PRAMYTFNHNKIISVLYTIIVFFNPAIYCLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID  
30 NO: 413).

ATGAGAAATTTGAGTGGAGGCCATGTGCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC  
CTCCCTCCAGCTGCTCCTCTTTGTCTTTTTTTTGCAATTTACCTTCTGACATTGTTGGAGA  
ATGCACTTATTGTCTTACAATATGGCTTGCTCCAAGCCTTCATCGTCCCATGTACTTTTTC  
35 CTGGCCATCTCTCTTTCCTGGAGCTATGGTACATCAATGTCAACCATTCCTCGGCTCTTGGC  
AGCCTTCTTACCCAGGATGGTAGAGTCTCCTACGTAGGTTGCATGACCCAACTGTACTTC  
TTTATTGCCTTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGCTACCT  
GGCCATCTGTGGACCCCTCCTTTACCCTAGTCTCATGCCTTCCAGTCTGGCCACTCGCCTTG  
CTGCTGCCTCTTGGGGCAGTGGCTTCTTCAGCTCCATGATGAAGCTTCTTTTATTTCCCAA  
40 TTGTCTACTGTGGACCCAACATTATCAACCACTTTTTCTGTGATATTCCCCACTACTCAA  
CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCTTCTGGCCCTGGTGATG  
ATTCTACTCCCTCTATTGGCTGTGGTTTCATCATACTGCCATCATTGCAGCCATCCTGAG  
GATCCCTACGTCCAGGGGACGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG  
GTTGTTATCTACTACTCCTCCACTCTCTTACCTATGCACGGCCCCGGCCATGTACACCTT  
45 CAACCACAACAAGATTATCTCTGTGCTCTACACTATCATTGTACCATTCTTCAACCCAGCCA  
TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGGCCTTCAAGGAAGACAGTGATGGGCAGAT  
GTCATATCCTAGGGATGTTTCAGGACTGA (SEQ ID NO: 414).

**AOLFR222 sequences:**

50 MGQTNVTSWRDFVFLGFSSSGELQLLFALFLSLYLVTLSNVFIIAIRLDSHLHTPMYFLSFL  
SFSETCYTLGIIPRMLSLAGGDQAISYVGCAAQMFFSASWACTNCFLLAAMGFDRYVAICAPL  
HYASHMNPTLCAQLVITSFLTGYLFGGLMTLVIFHLSFCSSHEIQHFFCDTPPVLSLACGDTGPS  
ELRIFILSLVLLVSFFFITISYAYILAILRIPSAEGQKKAFSTCASHLTVVIIHYGCASFVYLRPK  
ASYSLERDQLIAMTYTVVTPLLNPIVYSLRTRAIQTALRNAFRGRLLGKG (SEQ ID NO: 415).

55

ATGGGGCAGACCAACGTAACCTCCTGGAGGGATTTTGTCTTCTGGGCTTCTCCAGTTCTG  
 GGGAGTTGCAGCTCCTTCTCTTTGCCTTGTTCCTCTCTGTATCTAGTCACTCTGACCAGC  
 AATGTCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCCATGTACCTCTT  
 CTTTCTCTCCTATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAATGCTCT  
 5 CTGGCCTGGCTGGGGGGGACCAGGCTATCTCCTATGTGGGCTGTGCTGCCCAGATGTTCTT  
 TTCTGCCTCATGGGCCTGTACTAACTGCTTCCTTCTGGCTGCCATGGGCTTTGACAGATATG  
 TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCCTCTGTGCCAGCT  
 GGTCATTACTTCCTTCTGACTGGATACCTCTTTGGACTGGGAATGACACTAGTTATTTTCC  
 ACCTCTCATTCTGCAGCTCCCATGAAATCCAGCACTTTTTTTGTGACACGCCACCTGTGCTG  
 10 AGCCTAGCCTGTGGAGATACAGGCCCGAGTGAGCTGAGGATCTTTATCCTCAGTCTTTTG  
 TCCTCTTGGTCTCCTTCTTCTTCATCACCATCTCCTACGCCTACATCTTGGCAGCAATACTG  
 AGGATCCCCCTCTGCTGAGGGGCGAGAAGAAGGCCTTCTCCACTTGTGCCTCGCACCTTACAG  
 TGGTCATTATTATTATGGCTGTGCTTCTTCTGTGCTGAGGCCCCAAAGCCAGCTACTCT  
 CTTGAGAGAGATCAGCTTATTGCCATGACCTATACTGTAGTGACCCCCCTCCTTAATCCCA  
 15 TTGTTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGAG  
 ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).

**AOLFR223 sequences:**

20 MEAANESSEGISFVLLGLTTPGQQRPLFVLFLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA  
 HLSFADLCFASVTPKMLANLLAHDHSISLAGCLTQMYFFALGVTDSCLLAAMAYDCYVAIR  
 HPLPYATRMSRAMCAALVGMWLVSHVHSLLYILLMARLSFCASHQVPHFFCDHQPLRLSCL  
 SDTHHIQLLIFTEGAADVTPFLILASYGAIAAAVLQLPSASGRRLRAVSTCGSHLAVVSLFYGT  
 VIAVYFQATSRREAEGWRVATVMYTVVTPMLNPIIYSLWNRDVQALRALLIGRRISASDS  
 (SEQ ID NO: 417).

25 ATGGAGGCTGCCAATGAGTCTTCAGAGGGAATCTCATTCGTTTTATTGGGACTGACAACAA  
 GTCCTGGACAGCAGCGGCTCTCTTTGTGCTGTTCTTGTCTTGTATGTGGCCAGCCTCCTG  
 GGTAATGGACTCATTGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT  
 TCCTGCTGGCCCACTGTCTTTGCTGACCTCTGTTTCGCCTCCGTCACTGTGCCAAAGATG  
 30 TTGGCCAACTTGTGGCCCATGACCACTCCATCTCGCTGGCTGGCTGCCTGACCCAAATGT  
 ACTTCTTCTTTGCCCTGGGGGTAAGTGATAGCTGTCTTCTGGCGGCCATGGCCTATGACTG  
 CTACGTGGCCATCCGGCACCCCCCTCCCTATGCCACGAGGATGTCCCGGGCCATGTGCGCA  
 GCCCTGGTGGGAATGGCATGGCTGGTGTCCACGTCCACTCCCTCCTGTATATCCTGTCTCA  
 TGGCTCGCTTGTCTTCTGTGCTTCCACCAAGTGCCCCACTTCTTCTGTGACCACCAGCCT  
 35 CTCTTAAGGCTCTCGTGCTCTGACACCCACCACATCCAGCTGCTCATCTTCACCGAGGGCG  
 CCGCAGTGGTGGTCACTCCCTTCTGCTCATCCTCGCCTCCTATGGGGCCATCGCAGCTGC  
 CGTGCTCCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGGCTGTGTCCACCTGTGGCTCCCAC  
 CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCATTGCAGTCTACTTCCAGGCCACATCCC  
 GACGCGAGGCAGAGTGGGGCCGTGTGGCCACTGTCATGTACACTGTAGTACCCCCATGC  
 40 TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGGCACTCCGAGCCCTTCT  
 CATTGGGCGAAGGATCTCAGCTAGTGACTCCTGA (SEQ ID NO: 418).

**AOLFR224 sequences:**

45 MGSFNTSFEDGFILVGFSDWPQLEPILFVFIFIFYSLTFLGNTIIHALSWLDLRLHTPMYFFLSHL  
 LDLCFTTSTVPQLLINLCGVDRITTRGGCVAQFLFIYALGSTECVLLVVMADFDRYAACVCRPLHY  
 MAIMHPHLCQTLAIASWGAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT  
 EAKMFVARVIVVAVPAALILGSYVHIAHAVLRVKSTAGRRKAFGTGSHLLVVFLFYGSAIYT  
 YLQSIHNYSEREGKFVALFYTIITPILNPLIYTLRNDVKALWKVLWRGRDSG (SEQ ID NO:  
 419).

50 ATGGGAAGTTTCAACACCAGTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATTGGC  
 CGCAACTGGAGCCCATCCTGTTTGTCTTTATTTTATTTTCTACTCCCTAACTCTCTTTGGC  
 AACACCATCATCATCGCTCTCTCCTGGCTAGACCTTCGGCTGCACACACCTATGTAATTCTT  
 TCTCTCTCATCTGTCCCTCCTGGACCTCTGCTTACCACCAGCACCGTGCCCCAGCTCCTGA  
 55 TCAACCTTTGCGGGGTGGACCGACCATCACCCGTGGAGGGTGTGTGGCTCAGCTCTTCAT  
 CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCCTGGTGGTGATGGCCTTTGACCGCTAT

GCTGCTGTCTGTCGTCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCCCT  
 GGCTATCGCCTCCTGGGGTGC GG GTTTCGTGAACTCTCTGATCCAGACAGGTCTCGCAATG  
 GCCATGCCTCTCTGTGGCCATCGACTGAATCACTTCTTCTGTGAGATGCCTGTATTTCTGAA  
 GTTGGCTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCGAGTCATAGT  
 5 CGTGGCTGTTCCCTGCAGCACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG  
 AGGGTGAAGTCAACGGCTGGGCGCAGAAAGGCTTTTGGGACTTGTGGGTCCCACTCCTA  
 GTAGTTTTCCTTTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATTATTC  
 TGAGCGTGAGGGAAAATTTGTTGCCCTTTTTATACTATAATTACCCCATCTCAATCCTC  
 TCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAGTACTATGGAGGG  
 10 GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

**AOLFR225 sequences:**

MENYNQTSTDFILLGLFPPSIIDLFFFILVIFILMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID  
 LNYISTIVPKMASDFLHGKNSISFTGCGIQSFFFLALGGAEALLASMA YDRYIAICFPLHYLIRM  
 15 SKRVCVLMITGSWIIGSINACAHTVYVLHIPYCRSRAINHFFCDVPAMVTLACMDTWVYEGTV  
 FLSATIFLVFPFIGISCSYGQVLFVYHMKSAEGRKKA YLTCSTHLTVVTFYYAPFVYTYLRPRS  
 LRSPTEDKVLAVFYTILTPMLNPHYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).

ATGGAAAATTACAATCAAACATCAACTGATTTTCATCTTATTGGGGCTGTTTCCACCATCAA  
 20 TAATTGACCTTTTCTTCTTCACTTCTATTGTTTTCATTTTCCCTGATGGCTCTAATTGGAAACC  
 TGTCCATGATTCTTCTCATCTTCTTGGACACCCATCTCCACACACCCATGTATTTCTACTG  
 AGTCAGCTCTCCCTCATTGACCTAAATTACATCTCCACCATTTGTTCTAAGATGGCATCTGA  
 TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTCAGAGTTTCTTCTTCT  
 TGGCATTAGGAGGTGCAGAAGCACTACTTTTGGCATCTATGGCCTATGATCGTTACATTGC  
 25 TATTTGCTTTTCTCTCCACTATCTCATCCGCATGAGCAAAAGAGTGTGTGTGCTGATGATA  
 ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTACTCCATA  
 TTCCTTATTGCCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCCAGCAATGGTGACT  
 CTGGCCTGCATGGACACCTGGGTCTATGAGGGGCACAGTGTTTTTGAGTGCCACCATCTTTC  
 TCGTGTITCCCTTCATTGGTATTTTCATGTTCCTATGGCCAGGTTCTCTTTGCTGTCTACCAC  
 30 ATGAAATCTGCAGAAGGGAGGAAGAAAGCCTATTTGACCTGCAGCACCCACCTCACTGTA  
 GTAACCTTCTACTATGCACCTTTTGTCTACACTTATCTACGTCCAAGATCCCTGCGATCTCC  
 AACAGAGGACAAGGTTCTGGCTGTCTTCTACACCATCCTCACCCCAATGCTCAACCCCATC  
 ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGCCCTGACACGAGTGAGTCAGAGAATC  
 TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).

**AOLFR226 sequences:**

MEWRNHSGRVSEFVLLGFPAPAPLQVLLFALLLLAYVLVTENTLIIMAIRNHSTLHKPMYFFL  
 ANMSFLEIYWYVTVTIPKMLAGFVGSQDHLISFEGCMTQLYFFLGLGCTECVLLAVMAYD  
 RYMAICYPLHYVIVSGRLCVQMAAGSWAGGFGISMVKVFLISGLSYCGPNIINHFFCDVSPLL  
 40 NLSCTDMSTAELTDFILAIFILLGPLSVTGASYVAITGAVMHISAAAGRYKAFSTCASHLTVVIIF  
 YAASIFIYARPKALSAFDTNKLVSVLYAVIVPLLNPIIYCLRNQEVKRALCCTLHLYQHQPDP  
 KKASRVN (SEQ ID NO: 423).

ATGGAGTGGCGGAACCATAGTGGGAGAGTGAGTGAGTTTGTGTTGCTGGGCTTCCCTGCT  
 45 CCTGCGCCACTACAGGTACTATTGTTTGCCTTTTGTGCTGGCCTATGTGTTGGTGCTGAC  
 TGAGAACACACTCATCATTATGGCAATTAGGAACCATCTACCCTCCACAAACCATGTAC  
 TTTTTCTAGCTAATATGTCCTTTCTGGAGATCTGGTATGTCACTGTCACTATTTCCCAAGAT  
 GCTTGCTGGCTTTGTTGGATCCAAACAGGATCATGGACAGCTAATCTCCTTTGAGGGATGC  
 ATGACACAGCTCTACTTTTTCTTGGCTTGGGCTGCACTGAGTGTGCTCCTTCTCGTGTAT  
 50 GGCTATGATCGCTATATGGCCATCTGCTATCCTCTCCACTACCCAGTCATTGTCAAGTGGCC  
 GGCTGTGTGTGCAGATGGCTGCTGGCTCTTGGGCTGGAGGTTTTGGCATCTCCATGGTCAA  
 AGTTTTTCTTATTTCTGGCCTCTCTTACTGTGGCCCCAACATCATCAACCACTTTTTCTGTG  
 ATGTCTCTCCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTC  
 ATCCTGGCCATTTTTATTCTTCTAGGGCCACTCTCTGTCACTGGGGCCTCCTATGTGGCCAT  
 55 TACTGGTGCTGTGATGCACATATCTTCGGCTGCTGGACGCTATAAGGCCTTTTCCACCTGT  
 GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCAGCCAGTATCTTCATCTATGCTCGGCC

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTACTGTATGCTGTCATTGTA  
CCATTGCTCAATCCCATCATTTACTGCCTGCGCAATCAAGAGGTCAAGAGAGCCCTATGCT  
GTACTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA  
G (SEQ ID NO: 424).

5

**AOLFR227 sequences:**

MEPQNTSTVTNLFQLLGFQNLLEWQALLFVIFLLIYCLTIHGNVVIITVVSQGLRLHSPMYMFLQH  
LSFLEVWYTSTTVPLLLANLLSWGQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP  
LRYPFMLHRGLCARLVVVSCTGVSTGFLHSMMSRDLFCGRNQINHFFCDLPLMLQLSCSRV  
10 YITEVTIFILSIAVLCICFFLTLPYVVFIVSSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMISMIV  
CPSPHLLPEINKIISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKCGILWSTSKRKF  
LY (SEQ ID NO: 425).

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTCAGCTGTTAGGATTCCAGAACCTTC  
15 TTGAATGGCAGGCCCTGCTCTTTGTCAATTTTCTGCTCATCTACTGCCTGACCATTATAGGG  
AATGTTGTCATCATCACCGTGGTGAGCCAGGGCCTGCGACTGCACTCCCTATGTACATGT  
TCCTCCAGCATCTCTCCTTTCTGGAGGTCTGGTACACGTCCACCACTGTGCCCCCTTCTCCTA  
GCCAACCTGCTGTCTGCGGCCAACCCATCTCCTTCTCTGCCTGCATGGCACAGCTCTACT  
TCTTCGTATTCTCGGCGCCACCGAGTGCTTTCTCTGCGCTTCATGGCCTATGACCGTTAC  
20 CTGGCCATCTGCAGCCCACTCCGCTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGTT  
GGTGGTGGTCTCATGGTGCACAGGGGTCAGCACAGGCTTTCTGCATTCCATGATGATTTCC  
AGGTTGGACTTCTGTGGGCGCAATCAGATTAACCATTTCTTCTGCGACCTCCCGCCACTCA  
TGCAGCTCTCCTGTTCCAGAGTTTATATCACCGAGGTGACCATCTTCATCCTGTCAATTGCC  
GTGCTGTGCATTTGTTTTTCTGACACTGGGGCCCTATGTTTTTCATTGTGTCTCCTCATATT  
25 GAGAATCCCTTCCACCTCTGGCCGGAGAAAGACCTTTTCCACATGTGGCTCCCACTGGCT  
GTTGTCACTCTCTACTACGGGACCATGATCTCCATGTATGTGTGTCCAGTCCCCACCTGTT  
GCCTGAAATCAACAAGATCATTTCTGTCTTCTACACTGTGGTACACCACTGCTGAACCCA  
GTTATCTACAGCTTGAGGAACAAAGACTTCAAAGAAGCTGTTAGAAAGGTCATGAGAAGG  
AAATGTGGTATTCTATGGAGTACAAGTAAAGGAAGTTCCTTTATTAG (SEQ ID NO: 426).

30

**AOLFR229 sequences:**

MFYVNQIPFQLYHISFVYPTELWSRAIIPCMPTLSFWVCSATPVSPGFFALILLVFVTSIASNVVK  
IILIHDSRLHTPMYFLLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAE  
FFLLGLMSCDRYVAICNPLHYPDLMSRKICWLIVAAA WLGGSIDGFLTPVTMQFPFCASREIN  
35 HFFCEVPALLKLSCTDTSAYETAMYVCCIMMLLPFSVISGSYTRILITVYRMSEAEGRRAKAVAT  
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVTGALQK  
VVGRCVSSGKVTTT (SEQ ID NO: 427).

ATGTTTTATGTAAATCAGATACCTTTCCAACCTTTATCATATCTCTTTCGTGTACCCTACAGA  
40 GCTATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTACGA  
ACGCCCCGTTTCCCCTGGCTTCTTTGCCCTCATTCTCCTGGTCTTTGTGACCTCCATAGCCAG  
CAACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTC  
CTGCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATGTGCCCAAAATGCT  
GGTCCGACCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCACTGCCCAACACTTC  
45 CTCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCTGTGATCGCTA  
CGTAGCCATCTGCAACCCTCTGCACTATCCTGACCTCATGAGCCGCAAGATCTGCTGGTTG  
ATTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCACCA  
TGCAGTTCCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTT  
CTGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGCTGTCTGTATTA  
50 TGATGCTCCTCATCCCTTTCTCTGTGATCTCGGGCTCTTACACAAGAATTCTCATTACTGTT  
TATAGGATGAGCGAGGCAGAGGGGAGGCGAAAGGCTGTGGCCACCTGCTCCTCACACATG  
GTGGTTGTACAGCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA  
CACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTCACTCCCATGCTCAAT  
CCTACTCATTTACAGCCTTAGGAACAAGGATGTCACGGGGGCCCTACAGAAGGTTGTTGGG  
55 AGGTGTGTGCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).

**AOLFR230 sequences:**

MGMEGLLQNSTNFVLTGLITHPAFPGLLFAIVFSIFVVAITANLVMILLIHMD SRLHTPMYFLLS  
QLSIMDTIYICITVPKMLQDLLSKDKTISFLGCAVQIFLYLTLIGGEFFLLGLMAYDRYVAVCNP  
5 LRYPLL MNRRVCLFMVVG SWVGGSLDGFMLTPVTMSFPFCRSREINHFFCEIPAVLKL SCDTDS  
LYETLMYACCVLM LLIPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVVS VFYGAIFY  
TNVLPHSYHTPEKDKVVS AFYTILTPMLNPLIYSLRNKDVAALRKVLGRCGSSQSIRVATVIR  
KG (SEQ ID NO: 429).

10 ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTTCGTCCTCACAGGCCTCATCACCC  
ATCCTGCCTTCCCCGGGCTTCTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA  
GCCAACTTGGTCATGATTCTGCTCATCCACATGGACTCCCGCTCCACACACCCATGTACTT  
CTTGCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCAAGATGC  
TCCAGGACCTCCTGTCCAAGGACAAGACCATTTCCTTCCTGGGCTGTGCAGTTCAGATCTT  
15 CCTCTACCTGACCCTGATTGGAGGGGAATTCTTCCTGCTGGGTCTCATGGCCTATGACCGC  
TATGTGGCTGTGTGCAACCCTCTACGGTACCCTCTCCTCATGAACCGCAGGGTTTGCTTATT  
CATGGTGGTCCGGCTCCTGGGTGGTGGTTCCTGGATGGGTTCATGCTGACTCCTGTCCT  
ATGAGTTTCCCTTCTGTAGATCCCGAGAGATCAATCACTTTTTCTGTGAGATCCCAGCCGT  
GCTGAAGTTGTCTTGCACAGACACGTCACCTATGAGACCCTGATGTATGCCTGCTGCGTG  
CTGATGCTGCTTATCCCTCTATCTGTCTCTCTGTCTCCTACACGCACATCCTCCTGACTGT  
20 CCACAGGATGAACTCTGCTGAGGGCCGGCGCAAAGCCTTTGCTACGTGTTCTCCACATT  
ATGGTGGTGAGCGTTTTCTACGGGGCAGCCTTCTACACCAACGTGCTGCCCCACTCCTACC  
ACACTCCAGAGAAAGATAAAGTGGTGTCTGCCTTCTACACCATCCTACCCCCATGCTCAA  
CCCACTCATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGG  
GAGATGTGGTTCCTCCCAGAGCATCAGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID  
25 NO: 430).

**AOLFR231 sequences:**

MERANHSVVSEFILLGLSKSQNLQILFFLGFSVVFVGIVLGNLLILVTVTFDSLHHTPMYFLLSNL  
SCIDMILASFATPKMIVDFLRERKTISWWGCYSQMFFMHLLGGSEMMLLVAMAIDRYVAICKP  
30 LHYMTIMSPRVL TGLLLSSYAVGVFHSSSQMAFMLTLPFCGPNVIDSFFCDLPLVIKLACKDTYI  
LQLLVIADSGLLSLVCFLLLLVSYGVIFSVRYRAASRSSKAFSTLSAHITVTLFFAPCVFIYVW  
PFSRYSVDKILSVFYTIFTPLNPIIYTLRNQEVKAAIKRLCI (SEQ ID NO: 431).

35 ATGGAAAGAGCAAACCATT CAGTGGTATCGGAATTTATTTTGTGGGACTTTCCAAATCTC  
AAAATCTTCAGATTTTATTCTTCTTGGGATTCTCTGTGGTCTTCGTGGGGATTGTGTTAGGA  
AACCTGCTCATCTTGGTGACTGTGACCTTTGATTGCTCCTTCACACACCAATGTATTTTCT  
GCTTAGCAACCTCTCCTGCATTGATATGATCCTGGCTTCTTTTGCTACCCCTAAGATGATTG  
TAGATTTCTCCTCCGAGAACGTAAGACCATCTCATGGTGGGGATGTTATTTCCAGATGTTCTT  
TATGCACCTCCTGGGTGGGAGTGAGATGATGTTGCTTGTAGCCATGGCAATAGACAGGTAT  
40 GTTGCCATATGCAAACCCCTCATTACATGACCATCATGAGCCACGGGTGCTCACTGGGC  
TACTGTTATCCTCCTATGCAGTTGGATTTGTGCACTCATCTAGTCAAATGGCTTTTATGTTG  
ACTTTGCCCTTCTGTGGTCCCAATGTTATAGACAGCTTTTTCTGTGACCTTCCCTTGTGAT  
TAAACTTGCCTGCAAGGACACCTACATCTACAGCTCCTGGTCATTGCTGACAGTGGGCTC  
CTGTCACTGGTCTGCTTCTCCTCTTGTCTCTCCTATGGAGTCATAATATTCTCAGTTAG  
45 GTACCGTGCTGCTAGTCGATCCTCTAAGGCTTTCTCCACTCTCTCAGCTCACATCACAGTTG  
TGACTCTGTTCTTTGCTCCGTGTGTCTTTATCTACGTCTGGCCCTTCAGCAGATACTCGGTA  
GATAAAATTCTTTCTGTGTTTTACACAATTTTACACCTCTCTTAAATCCTATTATTATAC  
ATTAAGAAATCAAGAGGTAAGAGCAGCCATTAAAAAAGACTCTGCATATAA (SEQ ID NO:  
432).

**AOLFR232 sequences:**

MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV  
VIFVFLMALSGNAVILLIHCD AHLHTPMYFFISQLSLMDMAYISVTVPKMLLDQVMGVN KIS  
APEGCMQMFFYVTLAGSEFFLLATMAYDRYVAICHPLRYPVLMNHRVCLFLSSGCWFLGSVD  
55 GFTFTPTMTFPFRGSREIHFFCEVPAVLNLSCSDTSLYEIFMYLCCVLM LLI PVVIISSSYLLILL



TIHGMNSAEGRKKAFATCSSHLTVVILFYGAAIYTYMLPSSYHTPEKDDMMVSVFYTILTPVVNP  
LIYSLRNKDVIMGALKKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTCGGATTTCATCCTGATGGGAC  
TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCCAACCACACTGGATG  
GTCGGATTTCATCCTGTTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG  
GTCATTTTTGTGGTTTTCTGATGGCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACA  
CTGTGACGCCCCACCTCCACACCCCCATGTACTTTTTCATCAGTCAATTGTCTCTCATGGACA  
TGGCGTACATTTCTGTCACTGTGCCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAA  
10 GATCTCAGCCCCTGAGTGTGGGATGCAGATGTTCTTCTACGTGACACTAGCAGGTTTCAGAA  
TTTTTCCTTCTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTA  
CCCTGTCTCATGAACCATAGGGTGTGTCTCTTCTGTCTCATCAGGCTGCTGGTTCCTGGGCT  
CAGTGGATGGCTTCACATTCACCTCCCATCACCATGACCTTCCCCTTCCGTGGATCCCGGA  
GATTCATCATTTCTTCTGTGAAGTTCCTGCTGTATTGAATCTCTCCTGCTCAGACACCTCAC  
15 TCTATGAGATTTTTCATGTACTTGTGCTGTCTCATGCTCCTCATCCCTGTGGTGTATCAT  
TCAAGCTCCTATTTACTCATCCTCTCCTCACCATCCACGGGATGAAGTACGACAGAGGGCCGGA  
AAAAGGCCTTTGCCACCTGCTCCTCCACCTGACTGTGGTTCATCCTCTTCTATGGGGCTGCC  
ATCTACACCTACATGCTCCCCAGCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTG  
TCTTCTATACCATCCTCACTCCAGTGGTGAACCTTTAATCTATAGTCTTAGGAATAAGGAT  
20 GTCATGGGGGCTCTGAAGAAAATGTAAACAGTGGAACCTGCCTTTCAAAAAGCTATGGAG  
TAG (SEQ ID NO: 434).

**AOLFR233 sequences:**

25 MANITRMANHTGKLDIFILMGLFRRSKHPALLSVVIFVFLKALSGNAVLILLIHCDALHSPMY  
FFISQLSLMDMAYISVTVPKMLLDQVMGVNKSVAPECGMQMFLYLTLAGSEFFLLATMAYDR  
YVAICHPLRYPVLMNHRVCLFLASGCWFLGSVDGFMLTPITMSFPFCRSWEIHFFCEVPAVTI  
LSCSDTSLYETLMYLCCVLMLLIPVTIHSYLLILLTVHRMNSAEGRKKAFATCSSHLTVVILFY  
GAAVYTYMLPSSYHTPEKDDMMVSVFYTILTPVLNPLIYSLRNKDVIMGALKKMLTVRFVL  
(SEQ ID NO: 435).  
30 ATGGCCAACATCACCGGATGGCCAACCACACTGGAAAGTTGGATTTCATCCTCATGGGAC  
TCTTCAGACGATCCAAACATCCAGCTCTACTAGTGTGGTCATCTTTGTGGTTTTCTGAAG  
GCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACACTGTGACGCCCCACCTCCACAGCC  
CCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG  
35 CCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAAGGTCTCAGCCCCCTGAGTGTGGG  
ATGCAGATGTTCTCTATCTGACACTAGCAGGTTTCGGAATTTTTCTTCTAGCCACCATGGC  
CTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTACCCTGTCTCATGAACCATAGG  
GTCTGTCTTTTCTGGCATCGGGCTGCTGGTTCCTGGGCTCAGTGGATGGCTTCATGCTCAC  
TCCCATCACCATGAGCTTCCCCTTCTGCAGATCCTGGGAGATTCATCATTCTTCTGTGAAG  
40 TCCCTGCTGTAACGATCCTGTCTGCTCAGACACCTCACTCTATGAGACCCCTCATGTACCTA  
TGCTGTGTCCTCATGCTCCTCATCCCTGTGACGATCATTTCAAGCTCCTATTTACTCATCCT  
CCTCACCGTCCACAGGATGAAGTACGACAGAGGGCCGAAAAAGGCCTTTGCCACCTGCTC  
CTCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCCGTCTACACCTACATGCTCCCCA  
GCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCCTCACTCC  
45 GGTGCTGAACCTTTAATCTATAGTCTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAA  
ATGTTAACTGTGAGATTCGTCTTTAG (SEQ ID NO: 436).

**AOLFR234 sequences:**

50 MPNSTTVMFEFLMRFSVDVWTLQILHSASFFMLYLVTLMGNILIVTVTCDSSLHMPMYFFLRN  
LSILDACYISVTVPTSCVNSLLDSTTISKAGCVAQVFLVFFVYVELLFLTIMAHDYVAVCQPL  
HYPVIVNSRICIQMTLASLLSGLVYAGMHTGSTFQLPFCRSNVIHQFFCDIPSLLKLSCSDTFSNE  
VMIVVSALGVGGGCFIFIRSYIHIFSTVLGFPRGADRTKAFSTCIPHILVVSFLSSCSSVYLRPP  
AIPAATQDLILSGFYSIMPLFNPIYSLRNKQIKVAIKKIMKRIFYSENV (SEQ ID NO: 437).  
55 ATGCCCAATTCAACCACCGTGATGGAATTTCTCCTCATGAGGTTTTCTGATGTGTGGACAC  
TACAGATTTTACATTCTGCATCCTTCTTTATGTTGTATTTGGTAACTCTAATGGGAAACATC

CTCATTGTGACCGTCACCACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCCTCAG  
 GAATCTGTCTATCTTGGATGCCTGCTACATTTCTGTTACAGTCCCTACCTCATGTGTCAATT  
 CCCTACTGGACAGCACCACCATTCTAAGGCGGGATGTGTAGCTCAGGTCTTCTCGTGGT  
 TTTTTTGTATATGTGGAGCTTCTGTTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG  
 5 TCTGCCAGCCACTTCACTACCCTGTGATCGTGAACCTCTCGAATCTGCATCCAGATGACACT  
 GGCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG  
 CCCTTCTGTGCGTCCAACGTTATTCATCAATTCTTCTGTGACATCCCCTCTCTGCTGAAGCT  
 CTCTTGCTCTGACACCTTCAGCAATGAGGTCATGATTGTTGTCTCTGCTCTGGGGGTAGGT  
 GGCGGCTGTTTCATCTTTATCATCAGGTCTTACATTACATCTTTTCGACCGTCTCGGGTT  
 10 TCCAAGAGGAGCAGACAGAACAAGGCCTTTTCCACCTGCATCCCTCACATCCTGGTGGTG  
 TCAGTCTTCTCAGTTCATGCTCTTCTGTGTACCTCAGGCCACCTGCGATACCTGCAGCCAC  
 CCAGGATCTGATCCTTTCTGGTTTTTATTCCATAATGCCTCCCCTCTTTAACCTATTATTTA  
 CAGTCTTAGAAATAAGCAAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAATTTTTTA  
 TTCAGAAAATGTGTAA (SEQ ID NO: 438).

15

**AOLFR235 sequences:**

MDGVNDSSLQGFVLMGISDHPQLEMIFFIALLFSYLLTLLGNSTHLLSRLEARLHTPMYFFLSNL  
 SSLLAFATSSVPQMLINLWGPCKTISYGGCITQLYVFLWLGATECILLVMAFDTRYVAVCRPL  
 RYTAIMNPQLCWLLAVIACLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL  
 20 NQAVLNGVCTFFTA VPLSIHVISYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVFLFYGSASYGY  
 LLPAKNSKQDQGFISLFYSLVTPMVNPLIYTLRNMEVKGALRRLGKGREVG (SEQ ID NO:  
 439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC  
 25 CCCAGCTGGAGATGATCTTTTTTATAGCCATCCTCTTCTCCTATTTGCTGACCCTACTTGGG  
 AACTCAACCATCATCTTGCTTTCCCGCTGGAGGCCCGGCTCCATACACCCATGTACTTCTT  
 CCTCAGCAACCTCTCCTCCTTGGACCTTGCTTTTCGCTACTAGTTCAGTCCCCCAAATGCTGA  
 TCAATTTATGGGGACCAGGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT  
 CTTCTTTTGGCTGGGGGCCACCGAGTGCATCCTGCTGGTGGTGATGGCATTGACCGCTAC  
 30 GTGGCAGTGTGCCGGCCCCCTCCGCTACACCGCCATCATGAACCCCCAGCTCTGCTGGCTGC  
 TGGCTGTGATTGCCTGCCTGGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCACCTCT  
 GCAGTCCCATTTGTGTGGGCACCGGAGGGTGGAGGGATTCTCTGCGAGGTGCCTGCCAT  
 GATCAAACTGGCCTGTGGCGACACAAGTCTCAACCAGGCTGTGCTCAATGGTGTCTGCACC  
 TTCTTCACTGCAGTCCCACTAAGCATCATCGTGATCTCCTACTGCCTCATTGCTCAGGCAGT  
 35 GCTGAAAATCCGCTCTGCAGAGGGGAGGCGAAAGGCGTTCAATACGTGCCTCTCCCATCT  
 GCTGGTGGTGTTCCTCTTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGGCCAAGAAC  
 AGCAAACAGGACCAGGGCAAGTTCATTTCCCTGTTCTACTCGTTGGTCACACCCATGGTGA  
 ATCCCCTCATCTACACGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTTGCTGG  
 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

40

**AOLFR236 sequences:**

MTSQERDTAIYSINVSFVAKGMTSRVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL  
 LFLLIYSITVAGNLLILLTVGSDSHLSLPMYHFLGHL SFLDACLSTVTPKVMAGLLTLDGKVIS  
 FEGCAVQLYCFHFLASTECFLYTVMAYDRYLAICQPLHYPVAMNRRMCAEMAGITWAIGATH  
 45 AAIHTSLTFRLLYCGPCHIA YFFCDIPPVLKLACTDTTINELVMLASIGIVAAGCLILIVISYIFIVA  
 AVLRI RTAQGRQRAFSPCTAQLTGVLVYYVPPVCIYLQPRSSEAGAGAPAVFYTIVTPMLNPFYI  
 TLRNKEVKHALQRLLCSSSFRESTAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCCATTAATGTCAGTTTTGTTGCAAAGG  
 50 GGATGACTAGCCGCTCTGTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCAGA  
 CTGTGGTGAGCCACTTCTTCTGGAGGGTTGAGGTACACCGCTAAACATTCTAGCCTCTT  
 CTTCTCTCTTCTCCTCATCTACAGCATCACTGTGGCTGGGAATCTCCTCATCCTCCTAA  
 CTGTGGGCTCTGACTCTCACCTCAGCTTACCCATGTACCACTTCTGGGGCACCTCTCCTTC  
 CTGGATGCCTGTTTGTCTACAGTGACAGTGCCCAAGGTCATGGCAGGCCTGCTGACTCTGG  
 55 ATGGGAAGGTGATCTCCTTTGAGGGCTGTGCCGTACAGCTTTATTGCTTCCACTTTCTGGC  
 CAGCACTGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

5 CCCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC  
 TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTCACCTTCCGCCTGCTCTACT  
 GTGGGCCCTTGCCACATTGCCTACTTCTTCTGCGACATAACCCCTGTCCTAAAGCTCGCCTGT  
 ACAGACACCACCATTAATGAGCTAGTCATGCTTGCCAGCATTGGCATCGTGGCTGCAGGCT  
 10 GCCTCATCCTCATCGTTATTTCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA  
 GCCCAGGGCCGGCAGCGGGCCTTCTCCCCCTGCACTGCCAGCTCACTGGGGTGCTCCTGT  
 ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGGC  
 CCCTGCTGTCTTCTACACAATCGTAACTCCAATGCTCAACCCATTCAATTTACACTTTGCGGA  
 ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAGCAGCTTCCGAGAGTCTACAG  
 15 CAGGCAGCCACCCCATAG (SEQ ID NO: 442).

**AOLFR237 sequences:**

MDQRNYTRVKEFTFLGITQSRELSQVLFTFLFLVYMTTLMGNFLIMVTVTCESHLHTPMYFLL  
 15 RNLSILDICFSSITAPKVLIDLSETKTISFSGCVTQMFFHLLGGADVFSLSVMAFDRIAISKPL  
 HYMTIMSRGRCTGLIVGFLGGGLVHSIAQISLLPLPVCNVLDTFYCDVPQVLKLACTDFT  
 LELLMISNGLVSWFVFFLLISYTVILMMLRSHTEGRRKAISTCTSHITVTLHFVPCIYVYA  
 RPF TALPTDTAISVTFTVISPLLNPIIYTLRNQEMKLAMRKLKRRLLGQSERILIQ (SEQ ID NO:  
 443).  
 20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCCTGGGAATTACTCAGTCCC  
 GAGAACTGAGCCAGGTCTTATTTACCTTCCTGTTTTTGGTGTACATGACAACTCTAATGGG  
 AAACCTCCTCATCATGGTTACAGTTACCTGTGAATCTACCTTCATACGCCCCATGTACTTCC  
 TGCTCCGCAACCTGTCTATTCTTGACATCTGCTTTTCTCCATCACAGCTCCTAAGGTCCTG  
 ATAGATCTTCTATCAGAGACAAAAACCATCTCCTTCAGTGGCTGTGTCACTCAAATGTTCT  
 25 TCTTCCACCTTCTGGGGGGAGCAGACGTTTTTCTCTCTGTGATGGCGTTTGACCGCTAT  
 ATAGCCATCTCCAAGCCCCTGCACTATATGACCATCATGAGTAGGGGGCGATGCACAGGCC  
 TCATCGTGGGCTTCTGGGTGGGGGGCTTGTCCTACTCCATAGCGCAGATTTCTCTATTGCT  
 CCCACTCCCTGTCTGTGGACCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCC  
 TCAAACCTGCCTGCACTGACACCTTCACTCTGGAGCTCCTGATGATTTCAAATAATGGGTT  
 30 AGTCAGTTGGTTTGTATTCTTCTTCTCCTCATATCTTACACGGTCATCTTGATGATGCTGA  
 GGCTCACACTGGGGAAGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCCACATCACCG  
 TGGTGACCCTGCATTTCTGTCCTGTCATCTATGTCTATGCCCCGGCCCTTCACTGCCCTCCCC  
 ACAGACACTGCCATCTCTGTACCTTCACTGTCTATCTCCCCTTTGCTCAATCCTATAATTTA  
 CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAAACTGAAGAGACGGCTAGGAC  
 35 AATCAGAAAGGATTTTAATTCAATAA (SEQ ID NO: 444).

**AOLFR238 sequences:**

MAPENFTRVTEFILTGVSSCPQLIPLFLVFLVYVLTMAAGNLGIITLTSVDSRLQTPMYFFLRHL  
 40 AIINLGNSTVIAPKMLMFLVKKKTTSFYECATQLGGFLFFIVSEVMMLAVMAYDRYVAICNP  
 LLYMVVVSRRCLLLVSLTYLYGFSTAIIVSPCIFSVSYCSSNIINHFCYCDIAPLLALSCSDTYPE  
 TIVFISAATNLFMSMITVLVSYFNIVLSILRIRSPGRKKAFTCASHMIAVTVFYGTMLFMYLQP  
 QTNHSLDTDKMASVFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:  
 445).  
 45 ATGGCTCCTGAAAATTTACACAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC  
 CAGAGCTCCAGATTCCCCTCTTCTGGTCTTCTAGTGCTCTATGTGCTGACCATGGCAGG  
 GAACCTGGGCATCATCACCTCACAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT  
 TCCTGAGACATCTAGCTATCATCAATCTTGCAACTCTACTGTCATTGCCCTAAAATGCTG  
 ATGAACCTTTTATGTAAGAAGAAAACTACCTCATTCTATGAATGTGCCACCAACTGGGAG  
 50 GGTCTTGTCTTTATTGTATCGGAGGTAATGATGCTGGCTGTGATGGCCTATGACCGCTA  
 TGTGGCCATTTGTAACCTCTGCTCTACATGGTGGTGTCTCGGCGGCTCTGCCTCCTGC  
 TGGTGTCCCTCACGTACCTCTATGGCTTTTCTACAGCTATTGTGGTTTACCTTGTATATTC  
 TCTGTGCTTATTGCTCTTCTAATAATCAATCATTTTACTGTGATATTGCACCTCTGTT  
 AGCATTATCTTGCTCTGATACTTACATAACAGAAACAATAGTCTTTATATCTGCAGCAACA  
 55 AATTTGTTTTTTCCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTTGTCCATTCTA  
 AGGATACGTTACACAGAAGGAAGGAAAAAGCCTTTTCCACCTGCGCTTCGCATATGATA

GCAGTCACGGTTTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT  
CACTGGATACTGATAAGATGGCTTCTGTGTTTTACACATTGGTGATTCCTATGCTGAATCC  
CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAT  
CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

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**AOLFR239 sequences:**

MDPQNYSLVSEFVLHGLCTSRHLQNFFFIFFGVYVAIMLGNLLILVTVISDPCLHSSPMYFLLG  
NLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMQIFLHFTGGAEMVLLVSMAYDRYVAIC  
KPLHYMTLMSWQTCIRLVLASWVGVFVHSISQVAFTVNLPHYCGPNEVDSFFCDLPLVIKLACM  
10 DTYVLGIHMISDSGLLSLSCFLLLLISYTVILLAIRQRAAGSTSKALSTCSAHIMVVTLFFGPCIFV  
YVRPFSRFSVDKLLSVFYTIFTPLLNPIIYTLRNEEMKAAMKKLQNRRTVFQ (SEQ ID NO: 447).

ATGGACCCACAGAACTATTCCTTGGTGTCAGAATTTGTGTTGCATGGACTCTGCACTTCAC  
GACATCTTCAAAATTTTTCTTTATATTTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT  
15 AACCTTCTCATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACTCCTCCCTATGTA  
CCTGCTGGGGAACCTAGCTTTCCTGGACATGTGGCTGGCCTCATTTGCCACTCCCAAGATG  
ATCAGGGATTTCCTTAGTGATCAAAACTCATCTCCTTTGGAGGATGTATGGCTCAAATCT  
TCTTCTGCACTTACTGGTGGGGCTGAGATGGTGCTCCTGGTTTCCATGGCCTATGACAG  
ATATGTGGCCATATGCAAAACCCTTGCAATTACATGACTTTGATGAGTTGGCAGACTTGCATC  
20 AGGCTGGTGCTGGCTTCATGGGTCGTTGGATTTGTGCACTCCATCAGTCAAGTGGCTTTCA  
CTGTAAATTTGCCTTACTGTGGCCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG  
GTGATCAAACCTTGCCCTGCATGGACACCTATGTCTTGGGTATAATTATGATCTCAGACAGTG  
GGTTGCTTTCCTTGAGCTGTTTTCTGCTCCTCCTGATCTCCTACACCGTGATCCTCCTCGCT  
ATCAGACAGCGTGCTGCCGGTAGCACATCCAAAGCACTCTCCACTTGCTCTGCACATATCA  
25 TGGTAGTGACGCTGTTCTTTGGCCCTTGCAATTTTTGTTTATGTGCGGCCTTTTCA  
TCTGTGGACAAGCTGCTGTCTGTGTTTTATACCATTTTTACTCCACTCCTGAACCCCAT  
CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAAACCGACGGGT  
GACTTTTCAATGA (SEQ ID NO: 448).

**AOLFR240 sequences:**

MAGENHTTLPFLLLGFSDLKALQGPLFWVVLVYLVTLLGNSLIILLTQVSPALHSPMYFFLR  
QLSVVELFYTTDIVPRTLNLGSPHPQAISFQGCAAQMYVFIVLGISECCLLTAMAYDRYVAIC  
QPLRYSTLLSPRACLAMVGSSWLTGIITATTHASLIFSLPFRSHPIPHFLCDILPVLRLASAGKHR  
SEISVMTATIVFIMIPFSLIVTSYIRILGAILAMASTQSRKVFSTCSSHLLVVSFFGTASITYIRPQ  
35 AGSSVTTDRVLSLFYTVITPMLNPIIYTLRNKDVRRLRHLVKRQRPS (SEQ ID NO: 449).

ATGGCTGGGGAAAACCATACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA  
AGGCCCTGCAGGGCCCCCTGTTCTGGGTGGTGCTTCTGGTCTACCTGGTCACCTTGCTGGG  
40 TAACTCCCTGATCATCCTCCTCACACAGGTCAGCCCTGCCCTGCACTCCCCCATGTACTTCT  
TCCTGCGCCAACTCTCAGTGGTGGAGCTCTTCTACACCACTGACATCGTGCCAGGACCCT  
GGCCAATCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCCAGATG  
TACGTCTTCATTGTCTGGGCATCTCGGAGTGCTGCCTGCTCACGGCCATGGCCTATGACC  
GATATGTTGCCATCTGCCAGCCCCCTACGCTATTCCACCCTCTTGAGCCCCACGGGCCTGCTT  
GGCCATGGTGGGGTCTCCTGGCTCACAGGCATCATCACGGCCACCACCCATGCCTCCCTC  
45 ATCTTCTCTACCTTTTCGAGCCACCCGATCATCCCGCACTTTCTCTGTGACATCCTGCC  
AGTACTGAGGCTGGCAAGTGCTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGCCAC  
CATAGTCTTCATTATGATCCCCTTCTCTGATTGTACCTCTTACATCCGCATCCTGGGTG  
CCATCCTAGCAATGGCCTCCACCCAGAGCCGCCGCAAGGTCTTCTCCACCTGCTCCTCCCA  
TCTGCTCGTGGTCTCTCTCTTCTTTGGAACAGCCAGCATCACCTACATCCGGCCGCAAGGCA  
50 GGCTCCTCTGTTACCACAGACCGCGTCTCAGTCTCTTCTACACAGTCATCACACCCATGCT  
CAACCCCATCATCTACACCCTTCGGAACAAGGACGTGAGGAGGGCCCTGCGACACTTGGT  
GAAGAGGCAGCGCCCCCTCACCTGA (SEQ ID NO: 450).

**AOLFR241 sequences:**

MPQILIFTYLNMFYFFPPLQILAENLTMVTEFLLGFSSSLGEIQLALFVVFLLYLVILSGNVTHS  
VIHLDKSLHTPMYFFLGILSTSETFYTFVILPKMLINLLSVARTISFNCCALQMFFFLGFAITNCLL

LGVMGYDRYAAICHPLHYPTLMSWQVCGKLAACAIGGFLASLTVVNLVFSLPFCSANKVNH  
YFCDISAVILLACTNTDVNEFVIFICGVLVLVVPFLFICVSYLCILRTILKIPSAEGRRKAFSTCAS  
HLSVVIVHYGCASFIYLRPTANYVSNKDRLVTVTYITVTPLNPMVYSLRNKDVQLAIRKVLG  
KKGSLKLYN (SEQ ID NO: 451).

5

ATGCCCCAAATTCTTATATTACATACCTGAATATGTTTTACTTCTTTCCCCCTTTGCAGAT  
CTTGGCAGAAAACCTCACCATTGGTCACCGAATCCTGTTGCTGGGTTTTTCCAGCCTTGGT  
GAAATTCAGCTGGCCCTCTTTGTAGTTTTTCTTTTTCTGTATCTAGTCATTCTTAGTGGCAA  
TGTCACCATTATCAGTGTCTACACCTGGATAAAAGCCTCCACACACCAATGTACTTCTTCC  
10 TTGGCATTCTCTCAACATCTGAGACCTTCTACACCTTTGTCAATCTACCCAAGATGCTCATC  
AATCTACTTTCTGTGGCCAGGACAATCTCCTTCAACTGTTGTGCTCTTCAAATGTTCTTCTT  
CCTTGGTTTTGCCATTACCAACTGCCTGCTATTGGGTGTGATGGGTATGATCGCTATGCTG  
CCATTGTGTCACCTCTGCATTACCCCACTCTTATGAGCTGGCAGGTGTGTGGAAGAACTGGC  
AGCTGCCTGTGCAATTGGTGGCTTCTTGGCCTCTCTTACAGTAGTAAATTTAGTTTTACGCC  
15 TCCCTTTTTGTAGCGCCAACAAAGTCAATCATTACTTCTGTGACATCTCAGCAGTCATTCTT  
CTGGCTTGTACCAACACAGATGTTAAACGAATTTGTGATATTCAATTTGTGGAGTTCTTGTAC  
TTGTGGTTCCCTTTCTGTTTATCTGTGTTTCTTATCTCTGCATTCTGAGGACTATCCTGAAG  
ATTCCCTCAGCTGAGGGCAGACGGAAGCGTTTTCCACCTGCGCCTCTCACCTCAGTGTG  
TTATTGTTTATTATGGCTGTGCTTCTTCTATCTACCTGAGGCCTACAGCAAACTATGTGTCC  
20 AACAAAGACAGGCTGGTGACGGTGACATACAGATTGTCACTCCATTACTAAACCCCATG  
GTTTATAGCCTCAGAAACAAGGATGTCCAATGCTATCAGAAAAGTGTGGGCAAGAAA  
GGTTCTCTAAAACTATATAATTGA (SEQ ID NO: 452).

**AOLFR242 sequences:**

25 MNTTLFHPYSFLLLGPGLSMHLWVGPFPAVFLTAVLGNITLFIQTDSSLHHPMFYFLAILS  
SIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESAVLVAMAYDCYVAICDPLCY  
TLVLTNKKVSVMLAIFLRPLVFVIPFVLFILRLPFCGHQIIPHTYGEHMGRIARLSCASIRVNIY  
LCAISILVFDIIAIVISYVQILCAVFLSSHDARLKAFTSCGSHVCVMLTFYMPAFFSFMTHRFGR  
NIPHFHILLANFYVVIIPALNSVIYGVRTKQIRAVLKMFFNK (SEQ ID NO: 453).

30

ATGAATACCACTCTATTTTCATCCTTACTCTTTCTTCTTCTGGAATTCCTGGGCTGGAAG  
TATGCATCTCTGGGTGGTTTTCTTTCTTTGCTGTGTTCTGACAGCTGTCCTTGGGAATA  
TCACCATCCTTTTTGTGATTGAGACTGACAGTAGTCTCCATCATCCCATGTTCTACTTCTG  
GCCATTCTGTCTATCTATTGACCCGGGCTGTCTACATCCACCATCCCTAAAATGCTTGGCAC  
35 CTTCTGGTTTACCCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCCAGATGTTCTTCTATCC  
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC  
CATCTGTGACCTCTTTGCTACACGTTGGTGCTGACAAACAAGGTGGTGTGAGTTATGGCA  
CTGGCCATCTTTCTGAGACCTTAGTCTTTGTGCTATACCTTTGTTCTATTTATCCTAAGGCT  
TCCATTTTGTGGACACCAAAATTATCTCATACTTATGGTGAGCAGATGGGCATTGCCCCG  
40 CTGTCTTGTGCGCATCAGGGTTAATCATCATCTATGGCTTATGTGCCATCTCTATCCTGGT  
CTTTGACATCATAGCAATTGTCATTTCTATGTACAGATCCTTTGTGCTGTATTCTACTCT  
CTTCACATGATGCACGACTCAAGGCATTGACACCTGTGGCTCTCATGTGTGTGTCATGTT  
GACTTTCTATATGCCTGCATTTTTCTCATTATGACCCATAGGTTTGGTCGGAATATACCTC  
ACTTTATCCACATTCTTCTGGCTAATTTCTATGTAGTCATTCCACCTGCTCTCAACTCTGTA  
45 ATTTATGGTGTGAGAACCAACAGATTAGAGCACAAGTGCTGAAAATGTTTTCAATAAAT  
AA (SEQ ID NO: 454).

**AOLFR243 sequences:**

50 MEQVNTTVVREFVVLGFSSSLARLQQLLFVIFLLLYLFTLGTNMIISTIVLDRALHTPMYFFLAIL  
SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFFGSSHSFLAAMGYDRYMAICNPLR  
YSVLMGHGVCMLMAAACACGFTVSLVTTSLVFHLPHSSNQLHHFFCDISPVLKLASQHS  
SQLVIFMLGVFALVIPLLLLVSYIRIISAILKIPSSVGRYKTFSTCASHLIVTVHYSCASFIYLRPK  
TNYTSSQDTLISVSYTILTPLFNPMIYSLRNKEFKSALRRRTIGQTFYPLS (SEQ ID NO: 455).

55 ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTCGTCCTCGGCTTCTCATCCCTGG  
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCTGCTCCTCTACCTGTTCACTCTGGGCACC

AATGCAATCATCATTTCCACCATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT  
 CCTTGCCATCCTTTCTTGCTCTGAGATTTGCTATACCTTTGTCATTGTACCCAAGATGCTGG  
 TTGACCTGCTGTCCCAGAAGAAGACCATTCTTTCTGCTGGGCTGTGCCATCCAAATGTTTCC  
 TTCCTCTTCTTTGGCTCCTCTCACTCCTTCTGCTGGCAGCCATGGGCTATGATCGCTATAT  
 5 GGCCATCTGTAACCCACTGCGCTACTCAGTGCTCATGGGACATGGGGTGTGTATGGGACTA  
 ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCTCCCTGGTCACCACTCCCTAGTATTTCA  
 TCTGCCCTTCCACTCCTCCAACCAGCTCCATCACTTCTTCTGTGACATCTCCCCTGTCCTTA  
 AACTGGCATCTCAGCACTCCGGCTTCAGTCAGTGGTCATATTCATGCTTGGTGTATTGCT  
 CTTGGTCATTCTCTGCTACTTATCCTAGTCTCCTACATCCGCATCATCTCTGCCATTCTAA  
 10 AAATCCCTTCCCTCCGTTGGAAGATACAAGACCTTCTCCACCTGTGCCTCCCCTCATTGTG  
 GTAAGTGTCACTACAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATTACACTTC  
 AAGCCAAGACACCCTAATATCTGTGTACATACCATCCTTACCCCATTTGTTCAATCCAATG  
 ATTTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAACT  
 TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

15

**AOLFR244 sequences:**

MWQEYYFLNVFFPLLKVCCLTINSHVVILLPWECYHLIWKILPYIGTTVGSMEEYNTSSTDFTF  
 MGLFNKETSGLIFAIHSIFFTALMANGVMIFLIQTDLRLHTPMYFLLSHLSLIDMMYISTIVPKM  
 LVNYLLDQRTISFVGCTAQHFLYTLVGAEFFLLGLMAYDRYVAICNPLRYPVLMSSRVCWMI  
 20 IAGSWFGGSLDGFLLPITMSFPFCNSREINHFFCEAPAVLKLACADTALYETVMYVCCVLMML  
 IPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTVVSIFYGAAMYTYMLPHSYHKPAQ  
 DKVLSVFYITLTPMLNPLIYSLRNKDVGTALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

ATGTGGCAAGAATACTATTTTTTAAATGTTTTCTTCCCACTTTTAAAAGTTTGCTGCCTAAC  
 25 AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTTGGAAGATAT  
 TACCTTATATCGGCACAACGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT  
 CACTTTTCATGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTTGCCATCATCTCT  
 ATCATCTTCTTACCAGCACTGATGGCCAATGGGGTTATGATCTTCTGATCCAAACAGATT  
 TGCGCCTTCATACACCCATGTACTTCTCCTCAGCCACCTTTCCTTAATTGACATGATGTAT  
 30 ATTTCCACTATTGTGCCTAAGATGCTGGTTAATTACCTGCTGGATCAAAGGACCATTTCCTT  
 TGTGGGGTGCACAGCTCAACACTTCTCTACCTTACCCTTGTGGGAGCTGAATTCTTCTCTG  
 CTGGGCCTCATGGCCTATGACCGCTATGTGGCCATTGCAACCCTCTGAGATACCCTGTCC  
 TCATGAGCCGCCGGGTCTGTTGGATGATTATAGCAGGTTCCTGGTTTGGGGGCTCTTTGGA  
 TGGCTTCTCCTAACCCCATCACCATGAGCTTTCCTTCTGCAATTCCCGGGAGATTAAACC  
 35 ACTTCTTCTGTGAGGCACCAGCAGTCTGAAGTTGGCATGTGCAGACACAGCCCTCTACGA  
 GACAGTGATGTATGTGTGCTGTGTTTTGATGCTGCTGATTCTTTCTCTGTAGTCCTTGCTT  
 CCTATGCCCGAATCCTGACTACAGTTCAGTGCATGAGCTCAGTGGAGGGCAGGAAGAAGG  
 CATTTGCCACTGTCTCATCCCATGACTGTGGTGTCTTGTCTACGGGGCTGCCATGTAC  
 ACCTACATGCTGCCACATTCTTACCACAAGCCAGCCAGGACAAAGTCCTCTCTGTGTTTT  
 40 ACACCATTCCTCACACCCATGCTGAACCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC  
 TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCTCAAAGGGTGTGAGGAGGTGT  
 CTTTTGA (SEQ ID NO: 458).

**AOLFR245 sequences:**

MDLKNGLVTEFILLGFFGRWELQIFFVTFSLIYGATVMGNILIMVTVTCRSTLHSPLYFLLGN  
 45 LSFLDMCLSTATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLIIMAFDRYVAICKP  
 LHYRTIMSHKLLKGFAILSWIIGFLHSISQIVLTMNLPFCGHNVINNIFCDLPLVIKLACIETYTLE  
 LFVIADSGLLSFTCFILLVSYIVILVSVPKKSSHGLSKALSTLSAHIIIVTLFFGPCIFIYVWPFSSL  
 ASNKTALAVFYTVITPLLNPSIYTLRNKKMQEAIKRLRFQYVSSAQNF (SEQ ID NO: 459).

50

ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGGACGAT  
 GGGAACTTCAAATTTTCTTCTTGTGACATTTTCCCTGATCTACGGTGCTACTGTGATGGGA  
 AACATTCTCATTATGGTCACAGTGACATGTAGGTCAACCCTTCATTCTCCCTGTACTTTCT  
 CCTTGGAAATCTCTCTTTTTTGGACATGTGTCTCTCCACTGCCACAACACCCAAGATGATCA  
 55 TAGATTTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT  
 CATGCACTTCTTTGGGGGTGCTGAGATGACTCTTCTGATAATCATGGCCTTTGACAGGTAT

GTAGCCATATGTAAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG  
 TTTGCGATACTTTCATGGATAATTGGTTTTTTTACACTCCATAAGCCAGATAGTTTTAAACAAT  
 GAACTTGCCTTTCTGTGGCCACAATGTCATAAACAACATATTTTGTGATCTTCCCCTTGTGA  
 TCAAGCTTGCTTGCATTGAAACATACACCCTGGAATTATTTGTCAATTGCTGACAGCGGGCT  
 5 GCTCTCTTTCACCTGTTTCATCCTCTTGCTTGTTCCTTACATTGTCATCCTGGTCAGTGTACC  
 AAAAAAATCATCACATGGGCTCTCCAAGGCGCTGTCCACATTGCTGCCCACATCATTGTG  
 GTCACCTCTGTTCTTTGGACCTTGATTTTTATCTATGTTTGGCCATTGAGTAGTTTGGCAAG  
 CAATAAAACTCTTGCCGTATTTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA  
 CCCTGAGAAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCGAATATGTTAGTT  
 10 CTGCACAGAATTTCTAG (SEQ ID NO: 460).

**AOLFR246 sequences:**

MSPENQSSVSEFLLLGLPIRPEQQAVFFTLFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH  
 LALTDISFSSVTVPKMLMDMRTKYKSILYEECISQMYFFIFFTDLDSFLITSMAYDRYVAICHPL  
 15 HYTVIMREELCVFLVAVSWILSCASSLHTLLRLSFCFAANTIPHVFCDLAALLKLSCSDIFLNE  
 LVMFTVGVVITLPMFCILVSYGYIGATILRVPSTKGIHKALSTCGSHLSVSVSLYYGSIFGQYLF  
 PTVSSSIDKDVIVALMYTVVTPMLNPFYISLRNRDMKEALGKLFSRATFFSW (SEQ ID NO:  
 461).

20 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTTCTGGGCCTCCCCATCCGGC  
 CAGAGCAGCAGGCTGTGTTCTTACCCTGTTCTCTGGGCATGTACCTGACCACGGTGCTGGG  
 GAACCTGCTCATGCTGCTCATCCAGCTGGACTCTCACCTTCACACCCCCATGTACTTCT  
 TCCTCAGCCACTTGGCTCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG  
 ATGGACATGCGGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTTCTCAGATGTATT  
 25 TTTTTATAATTTTTACTGACCTGGACAGCTTCCTTATTACATCAATGGCATATGACCGATAT  
 GTTGCCATATGTCACCCTCTCCACTACACTGTCATCATGAGGGAAGAGCTCTGTGTCTTCTT  
 AGTGGCTGTATCTTGGATTCTGTCTTGTGCCAGCTCCCTCTCTCACACCCTTCTCCTGACCC  
 GGCTGTCTTTCTGTGCTGCGAACACCATCCCCATGTCTTCTGTGACCTTGCTGCCCTGCTC  
 AAGCTGTCTGTGCTCAGATATCTTCCCTCAATGAGCTGGTCATGTTTACAGTAGGGGTGGTGG  
 30 TCATTACCCTGCCATTTCATGTGTATCCTGGTATCATATGGCTACATTGGGGCCACCATCCTG  
 AGGGTCCCTTCAACCAAAGGGATCCACAAAGCATTGTCCACATGTGGCTCCCATCTCTCTG  
 TGGTGTCTCTCTATTATGGGTCAATATTTGGCCAGTACCTTTTCCCGACTGTAAGCAGTTCT  
 ATTGACAAGGATGTCATTGTGGCTCTCATGTACACGGTGGTCACACCCATGTTGAACCCCT  
 TTATCTACAGCCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAAACTCTTCAGTAGAG  
 35 CAACATTTTTCTCCTTGGTGACATCTGACTTTTTTAAAAAATTAG (SEQ ID NO: 462).

**AOLFR247 sequences:**

MGQHNLTVLTEFILMELTRPELQIPLFGVFLVIYLITVVGNLTMILTKLDSHLHTPMYFSIRHL  
 ASVDLGNSTVICPKVLANFVDRNTISYYACAAQLAFFLMFIIEFFILSAMA YDRYVAICNPLL  
 40 YYVIMSQRLLCHVLVGIQYLYSTFQALMFTIKIFTLTFCGSNVISHFYCDDVPLLPMLCSNAQEIE  
 LLSILFSVFNLISSFLIVLVS YMLILLAICQMHS AEGRKKAFSTCGSHLTVVVVFYGSLLFMYMQ  
 PNSTHFFDTDKMASVFYTLVIPMLNPLIYSLRNNEEVKNAFYKLFEN (SEQ ID NO: 463).

ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAACCTACAAGGCGGC  
 45 CTGAGCTGCAGATTCCCCTTTTTGGAGTCTTCCTCGTCATCTACCTAATCACAGTGGTGGGC  
 AACCTAACTATGATCATTGACCAAAGTGGACTCCCACTTACATACACCTATGTACTTTTC  
 TATCAGACATTTGGCTTCTGTTGATCTTGGTAATTCTACTGTCATTTGTCCCAAGGTGCTGG  
 CAAATTTTGTGTGGATCGAAATACTATTTCTATTATGCATGTGCTGCACAGCTGGCATTC  
 TTCCTTATGTTTATTATCAGTGAATTTTTCATCCTGTGAGCCATGGCCTATGACCGCTATGT  
 50 GGCCATTTGTAACCCTCTGCTCTATTATGTTATTATGTCTCAGCGACTGTGTCATGTACTGG  
 TGGGCATTCAATATCTCTACAGCACATTTTCAAGGCTCTGATGTTCACTATTAAGATTTTTACA  
 TTGACCTTCTGTGGCTCTAATGTCATCAGTCATTTTACTGTGATGATGTTCTTTGCTACC  
 TATGCTTTGCTCAAATGCACAGGAAATAGAATTGTTGAGCATACTATTTTCTGTATTTAAT  
 TGATCTCCTCCTTTCTGATAGTCTTAGTGTCCTACATGTTGATTTTGTAGCTATATGTCAA  
 55 ATGCAATTCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTTCCTATTTGACAGTGG  
 TGGTTGTGTTCTATGGGTCTCTACTCTTCATGTACATGCAGCCCAATTCCACTCACTTCTTT

GATACTGATAAAATGGCTTCTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCCTTTGAT  
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTGA  
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPALPTGGLLPHQPHTMMEIANVSSPEVFVLLGFSTRPSLETVLFIVVLSFYMVLSILNGNI  
IILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWL  
ATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGLTSMVGSTLTMLPLCG  
NNCIDHFFCEMLIMQLACVDTSLNEMEMYLASFVFFVPLGLILVSYGHIAVLRKIRSAEGR  
10 RKAFTNCSSHVAVVSLFYGSIIFFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTEVKS  
ALRHMVLENC CGSAGKLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCCACAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT  
GATGGAAATAGCCAATGTGAGTTCTCCAGAAGTCTTTGTCCTCCTGGGCTTCTCCACACGA  
15 CCCTCACTAGAACTGTCTCTTCATAGTTGTCTTGAGTTTTTACATGGTATCGATCTTGGG  
CAATGGCATCATCATTCTGGTCTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT  
TTCTTGCCAACTCCCTTCTGACATGAGCTTACCACGAGCATTGTCCCACAGCTCCTG  
GCTAACCTCTGGGGACCACAGAAAACCATAAGCTATGGAGGGTGTGTGGTCCAGTTCTAT  
ATCTCCCATTTGGCTGGGGGCAACCGAGTGTGTCTGCTGGCCACCATGTCTATGACCGCT  
20 ACGCTGCCATCTGCAGGCCACTCCATTACACTGTCATTATGCATCCACAGCTTTGCCTTGG  
GCTAGCTTTGGCCTCCTGGCTGGGGGGTCTGACCACCAGCATGGTGGGCTCCACGCTCACC  
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTTCTTTGCGAGATGCCCCCTCA  
TTATGCAACTGGCTTGTGTGGATACCAGCCTCAATGAGATGGAGATGTACCTGGCCAGCTT  
TGTCTTTGTTGCTGCTGCCTCTGGGGCTCATCCTGGTCTCTTACGGCCACATTGCCCGGGCCG  
25 TGTTGAAGATCAGGTCAGCAGAAGGGCGGAGAAAGGCATTCAACACCTGTTCTTCCCACG  
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTCATGTATCTCCAGCCAGCCAAGAG  
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTTCTACACCGTAGTCACTCCTGCGCTG  
AACCCACTTATTTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGCACATGGTA  
TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

30

**AOLFR249 sequences:**

MKSQIEKSDLKYRAILLQKVTRMFLLFWVLLLVLRLVVMGRGNSTEVTEFHLLGFGVQHEF  
QHVLFIVLLLIYVTSIGNIGMILLIKTDSRLQTPMYFFPQHAFVDICYTSAITPKMLQSFTEN  
NLITFRGCVIQLVYATFATSDCYLLAJMAMDCYVAICKPLRYPMIMSQT VYIQLVAGSYIIGSI  
35 NASVHTGFTFSLFCKSNKINHFFCDGLPILALSCSNIDINILDVVFGFDLMFTELVIIFSYIYIM  
VTILKMSSTAGRKKSFSSTCASHLTAVTIFYGTLSYMYLQPQSNNSQENMKVASIFYGTVIPMLN  
PLIYSLRNKEGK (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAGTGACTTAAATATAGAGCCATTTTATTGCAAAAAGTC  
40 ACAAGGATGTTCTGCTTTTCTGGGTCCTTCTCTTGGTCTTTCTAGACTTTTGGTAGTCAT  
GGGTCGAGGAAACAGCACTGAAAGTGAAGTGAATTCATCTTCTGGGATTTGGTGTCCAACAC  
GAATTTGAGCATGTCCTTTTCACTGACTTCTTCTTATCTATGTGACCTCCCTGATAGGAAA  
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTTCAAACACCCATGTACTTTTTTC  
CACAACATTTGGCTTTTGTGATATCTGTTATACTTCTGCTATCACTCCCAAGATGCTCCAA  
45 AGCTTCACAGAAGAAAATAATTTGATAACATTTGCGGGCTGTGTGATACAATTCTTAGTTT  
ATGCAACATTTGCAACCACTGACTGTTACCTCCTAGCTATTATGGCAATGGATTGTTATGT  
TGCCATCTGTAAGCCCTTCGCTATCCCATGATCATGTCCCAACAGTCTACATCCAACCTCG  
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTTACATTTTCA  
CTGTCTTCTGCAAGTCTAATAAAATCAATCACTTTTCTGTGATGGTCTCCCAATTCTTGC  
50 CCTTTCATGCTCCAACATTGACATCAACATCATTCTAGATGTTGTCTTTGTGGGATTTGACT  
TGATGTTCACTGAGTTGGTCATCATCTTTTCTACATCTACATTATGGTCACCATCCTGAAG  
ATGTCTTCTACTGCTGGGAGGAAAAAATCCTTCTCCACATGTGCCCTCCACCTGACAGCAG  
TAACCATTTTCTATGGGACACTCTTACATGTACTTACAGCCTCAGTCTAATAATTCTCAG  
GAGAATATGAAAGTAGCCTCTATATTTTATGGCACTGTTATTCCCATGTTGAATCCTTTAAT  
55 CTATAGCTTGAGAAATAAGGAAGGAAATAA (SEQ ID NO: 468).



**AOLFR250 sequences:**

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLIILAIGSDLHLHTPMYFFLANLSFV  
DMGLTSSTVTKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCY  
STVMRPQVCALMLALCWVLTNIVALHTHFLMARLSFCVTGEIAHFFCDITPVLKLSGSDTHINE  
5 MMVFLVGGTVLIVPFLCIVTSYIHIVPAILRVTRGGVGKAFSTCSSHL CVVCVFYGTFLFSAYLC  
PPSIASEEKDIAAAAMYTIVTPMLNPFYISLRNKDMKGALKRFLSHRSIVSS (SEQ ID NO: 469).

ATGGAAAACCAATCCAGCATTCTGAATTTTCTCCGAGGAATATCAGCGCCTCCAGAGC  
AACAGCAGTCCCTCTTCGGAATTTTCTGTGTATGTATCTTGTACCTTGACTGGGAACCTG  
10 CTCATCATCTCGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTTCTTGGC  
CAACCTGTCTTTTGTGACATGGGTTTAACGTCTCCACAGTTACCAAGATGCTGGTGAAT  
ATACAGACTCGGCATCACACCATCTCCTATACGGGTTGCCTCACGCAAATGTATTTCTTTCT  
GATGTTTGGTGATCTAGACAGCTTCTTCCTGGCTGCCATGGCGTATGACCGCTATGTGGCC  
ATTTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAATGCTTGC  
15 ATTGTGCTGGGTCTCACCAATATCGTTGCCCTGACTCACACGTTCTCATGGCTCGGTTGT  
CCTTCTGTGTGACTGGGGAAATTGCTCACTTTTCTGTGACATCACTCCTGTCTGAAGCTG  
TCATGTTCTGACACCCACATCAACGAGATGATGGTTTTTGTCTTGGGAGGCACCGTACTCA  
TCGTCCCTTTTATGCATTGTACCTCTACATCCACATTGTGCCAGCTATCCTGAGGGTC  
CGAACCCGTGGTGGGGTGGGCAAGGCCTTTTCCACCTGCAGTTCCACCTCTGCGTTGTTT  
20 GTGTGTTCTATGGGACCCTCTTCAGTGCCTACCTGTGTCTCCCTCCATTGCCTCTGAAGAG  
AAGGACATTGCAGCAGCTGCAATGTACACCATAGTACTCCCATGTTGAACCCCTTTATCT  
ATAGCCTAAGGAACAAGGACATGAAGGGGGCCCTAAAGAGGCTCTTCAGTCACAGGAGTA  
TTGTTTCTCTTAG (SEQ ID NO: 470).

**AOLFR251 sequences:**

MEGNKTWITDITLPRFQVGPAL EILLGLFSAFYTLTLLGNGVIFGIICLDCKLHTPMYFFLSHLA  
IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFAHVECLILVMSYDRYADICHPLRY  
NILMSWRVCTVLAVASWVFSLLALVPLVLRLPFCGPHEINHFEILSVLKLACADTWLNQV  
VIFAACVFILVGPLCLVLSYLRILAILRIQS GEGRRKAFSTCSSHL CVVGLFFGSAIVTYMAPK  
30 SRHPEEQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTTGGTCCA  
GCACTGGAGATTCTCCTCTGTGGACTTTTCTCTGCCTTCTATACACTCACCTGCTGGGGAA  
TGGGGTCATCTTTGGGATTATCTGCCTGGACTGTAAGCTTCACACACCCATGTACTTCTTCC  
35 TCTCACACCTGGCCATTGTTGACATATCCTATGCTTCCAACATATGTCCCAAGATGCTGACG  
AATCTTATGAACCAGGAAAGCACCATCTCCTTTTCCATGCATAATGCAGACATTCTTGT  
ATTTGGCTTTTGCTCACGTAGAGTGTCTGATTTTGGTGGTGATGTCCTATGATCGCTATGCG  
GACATCTGCCACCCCTTACGTTACAATATCCTCATGAGCTGGAGAGTGTGCACTGTCCTGG  
CTGTGGCTTCTGGGTGTTGAGCTTCTCCTGGCTCTGGTCCCTTTAGTTCTCATCTGAGG  
40 CTGCCCTTCTGCGGGCCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCTCAAGTT  
GGCCTGTGCTGACACCTGGCTCAACCAGGTGGTCATCTTTGCAGCCTGCGTGTTTCATCCTG  
GTGGGGCCACTCTGCCTGGTGCTGGTCTCCTACTTGCGCATCCTGGCCGCCATCTTGAGGA  
TCCAGTCTGGGGAGGGCCGCAGAAAGGCCTTCTCCACCTGCTCCTCCACCTTTGCGTGGT  
GGGACTCTTCTTGGCAGCGCCATTGTACGTACATGGCCCCCAAGTCCCGCCATCCTGAG  
45 GAGCAGCAGAAAGTTCTTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCTGA  
TATATAGCCTAAGGAATGCAGAGGTCAAGGGCGCCCTGAGGAGGGCACTGAGGAAGGAG  
AGGCTGACGTGA (SEQ ID NO: 472).

**AOLFR252 sequences:**

MRLANQTLGGDFFLLGIFSQISHPGRLCLLIFSIFLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL  
IDLTYSVTVPKMLVNQLAKDKTISVLGCGTQMYFYQLGGAECCLLAAMAYDRYVAICHPLR  
YSVLMSHRVCLLLASGCWFVGSVDGFMLTPIAMSFPCRSH EIQHFFCEVPAVLKLSGSDTSLY  
KIFMYLCCVIMLLIPVTVISVSYYYIILTIHKMNSVEGRKKAFTTCSHITVVSIFYGAAIYNYML  
55 PSSYQTPEKDMMSFFYTILTPVLNPIIYSFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

ATGCGGCTGGCCAACCAGACCCTGGGTGGTGACTTTTTCTGTTGGGAATCTTCAGCCAGA  
 TCTCACACCCTGGCCGCCTCTGCTTGCTTATCTTCAGTATATTTTGTATGGCTGTGTCTTGG  
 AATATTACATTGATACTTCTGATCCACATTGACTCCTCTCTGCATACTCCCATGTACTTCTT  
 5 TATAAACCACTCTCACTCATAGACTTGACATATATTTCTGTCACTGTCCCCAAAATGCTG  
 GTGAACCAGCTGGCCAAAGACAAGACCATCTCGGTCCTTGGGTGTGGCACCAGATGTAC  
 TTCTACCTGCAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCCATGGCCTATGACCGCT  
 ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC  
 CTGGCATCAGGCTGTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATCGCCA  
 10 TGAGCTTCCCCTTCTGCAGATCCCATGAGATTACAGCACTTCTTCTGTGAGGTCCCTGTGTT  
 TTGAAGCTCTCTTGCTCAGACACCTCACTTTACAAGATTTTCATGTACTTGTGCTGTGTCAT  
 CATGCTCCTGATACCTGTGACGGTCATTTCACTGTCTTACTACTATATCATCTCACCATCC  
 ATAAGATGAACTCAGTTGAGGGTCGGAAGGCTTCACCACCTGCTCCTCCACATTAC  
 AGTGGTCAGCCTCTTCTATGGAGCTGCTATTTACAACATACATGCTCCCACTCCTACCAA  
 ACTCCTGAGAAAGATATGATGTCATCCTTTTTCTACACTATCCTTACACCTGTCTTGAATCC  
 15 TATCATTTACAGTTTCAGGAATAAGGATGTCACAAGGGCTTTGAAAAAATGCTGAGCGT  
 GCAGAAACCTCCATATTAA (SEQ ID NO: 474).

**AOLFR253 sequences:**

20 MTFSSSGGNCEPVMCSGNQTSQNQTASTDFTLTGLFAESKHAALLYTVTFLLFLMALTGNALL  
 ILLIHSEPRLHTPMYFFISQALMDLMLYLCVTPKMLVGQVTGDDTISPSGCGIQMFFHLTLAG  
 AEVFLAAMAYDRYAACVRPLHYPLLMNQVRVCQLLSACWVLGMVDGLLTPITMSFPFCQS  
 RKILSFCETPALLKLSGSDVSLYKMLTYLCCILMLLTPIMVISSSYTLILHLIHRMNSAAGRRA  
 LATCSSHMIIVLLFGASFYTYMLRSSYHTAEQDMMVSAFYTIFTPVLNPLIYSLRNKDVTRAL  
 RSMMQSRMNQEK (SEQ ID NO: 475).

25 ATGACTTTTTTTTCTCAGGGGGAACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT  
 CTCAGAATCAAACAGCAAGCACTGATTTACCCCTCACGGGACTCTTGTGCTGAGAGCAAGCA  
 TGCTGCCCTCCTCTACACCGTGACCTTCTTCTTTCTTGTATGGCCCTCACTGGGAATGCC  
 30 TCTCATCCTCCTCATCCACTCAGAGCCCCGCTCCACACCCCCATGTACTTCTTCATCAGC  
 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCCAAGATGCTTGTGGGCC  
 AGGTCAGTGGAGATGATACCATTTCCCCGTCAGGCTGTGGGATCCAGATGTTCTTCCACCT  
 GACCTGGCTGGAGCTGAGGTTTTCTCCTGGCTGCCATGGCCTATGACCGATATGCTGCT  
 GTTTCAGACCTCTCCATTACCCACTGCTGATGAACCAGAGGGTGTGCCAGCTCCTGGTGT  
 CAGCCTGCTGGGTTTTGGGAATGGTTGATGGTTTGTGCTCACCCCCATTACCATGAGCTT  
 35 CCCCCTTGGCAGTCTAGGAAAATCCTGAGTTTTTCTGTGAGACTCCTGCCCTGCTGAAGC  
 TCTCCTGCTCTGACGTCTCCCTCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT  
 CTCACCCCCATCATGGTCATCTCCAGCTCATAACCCCTCATCCTGCATCTCATCCACAGGAT  
 GAATTCTGCCGCCGCCGAGGAAGGCTTGGCCACCTGCTCCTCCACATGATCATAGTG  
 CTGCTGCTCTTCGGTGCTTCTTCTACACCTACATGCTCCGGAGTCTTACCACACAGCTGA  
 40 GCAGGACATGATGGTGTCTGCCTTTTACACCATCTTCACTCCTGTGCTGAACCCCTCATTT  
 ACAGTCTCCGCAACAAAGATGTCACCAGGGCTCTGAGGAGCATGATGCAGTCAAGAATGA  
 ACCAAGAAAAGTAG (SEQ ID NO: 476).

**AOLFR254 sequences:**

45 MTNTSSSDFTLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI  
 MDTLFICTTVPKLLADMVSKEKISFVACGIQIFLYLTMIGSEFFLLGLMAYDCYVAVCNPLRYP  
 VLMNRKKCLLLAAGAWFGSLDGFLLPITMNVPCGSRNHHFCEIPAVLKLACADTSLEYET  
 LMYICCVLMLLIPISIHSTSYSLILLTIHRMPSAEGRKKAFTTCSHLLTVVSIFYGAIFYTYVLPQS  
 50 FHTPEQDKVVSIFYTIVTPMLNPLIYSLRNKDVIGAFKKVFACSSAQKVATSDA (SEQ ID NO:  
 477).

ATGACGAACACATCATCCTCTGACTTCACCCTCCTGGGGCTTCTGGTGAACAGTGAGGCTG  
 CCGGGATTGTATTTACAGTGATCCTTGCTGTTTTCTTGGGGGCCGTGACTGCAAATTTGGT  
 CATGATATTCTTGATTCAGGTGGACTCTCGCCTCCACACCCCCATGTACTTCTGCTCAGTC  
 55 AGCTGTCCATCATGGACACCTTTTCATCTGTACCACTGTCCCAAACTCCTGGCAGACAT  
 GGTTCATAAGAGAAGATCATTTCTTTGTGGCCTGTGGCATCCAGATCTTCTCTACCTG

ACCATGATTGGTTCTGAGTTCTTCCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT  
 CTGTAACCTCTGAGATACCCAGTCTGATGAACCGCAAGAAGTGTCTTTTGGCTGGCTGCT  
 GGTGCCTGGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCACCATGAATGTCC  
 CTTACTGTGGCTCCCGAAGTATCAACCATTTTTTCTGTGAGATCCCAGCAGTTCTGAAACT  
 5 GGCCTGTGCAGACACGTCCTTGTATGAAACTCTGATGTACATCTGCTGTGTCTCATGTTG  
 CTCATCCCCATCTCTATCATCTCCACTTCCTACTCCCTCATCTTGTTAACCATCCACCGCAT  
 GCCCTCTGCTGAAGGTCGCAAAAAGGCCTTACCACCTTGTTCCCTCCCACTTGACTGTAGTT  
 AGCATCTTCTATGGGGCTGCCTTCTACACATACGTGCTGCCCCAGTCTTCCACACCCCCG  
 10 AGCAGGACAAAGTAGTGTGAGCCTTCTATACCATGTGTCAGCCCATGCTTAATCCTCTCAT  
 CTACAGCCTCAGAAACAAGGACGTATAGGGGCATTAAAGGTATTTGCATGTTGCTCA  
 TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

**AOLFR255 sequences:**

MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKILLIHIDSRHTPMYFLLSQLS  
 15 LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH  
 YPVLMSRKICWLIVAAA WLGGSIDGFLTPVTMQFPFCASREINHFFCEVPALLKLSCTDTSAY  
 ETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRGKAVATCSSHMVVVSLFYGAAMYT  
 YVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQKVVGRCVSSGKVTTT (SEQ  
 ID NO: 479).

20 ATGGAGCAGAGCAATTATTCGGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCAACG  
 CCCGTTTCCCCTGGCTTCTCTTTGCCCTCATTCTCCTGGTCTTTTGACCTCCATAGCCAGC  
 AACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCTCCACACCCCCATGTACTTCTC  
 GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCCAAAATGCTG  
 25 GTCGACCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCACTGCCCAACACTTCC  
 TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCCTATGATCGCTAC  
 GTAGCCATCTGCAACCCTCTGCACTATCCTGTCTCATGAGCCGCAAGATCTGCTGGTTGA  
 TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCAACCAT  
 GCAGTTCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTC  
 30 TGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTAT  
 GATGCTCCTCATCCCTTTCTCTGTCTATCTCGGGCTCTTACACAAGAATTCTCATTACTGTTT  
 ATAGGATGAGCGAGGCAGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCTCACACATGG  
 TGGTTGTGACGCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCAC  
 ACCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTTACTCCCATGCTCAATC  
 35 CACTCATTTACAGCCTTAGGAACAAGGATGTACAGGGGCCCTACAGAAGGTTGTGGGGA  
 GGTGTGTGCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

**AOLFR256 sequences:**

MGGKQPWVTEFILVGFQVGPALAILLCGLFSVFYTLTLGNGVIFGIICLDSKLHTPMYFFLSHL  
 40 AIIDMSYASNNVPKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVMSYDRYVAICHPF  
 QYTVIMSWRVCTILASTCWIIISFLMALVHIITHILRPPFCGPQKINHFIQIMSVFKLACAGPRLNQ  
 VVLYAGSAFIVEGPLCLELVSNLHILSRHLEDPMGRAADRLTLPAPSHLCMVGLLFGSTMVM  
 YMAPKSRHPPEEQKVLSLFYSLFNPMNLPLIYSLRNAEYKALKRVLWKQRSK (SEQ ID NO:  
 481).

45 ATGGGAGGCAAGCAGCCCTGGGTACAGAATTCATCCTGGTGGGATTCCAGGTTGGTCCA  
 GCACTGGCGATTCTCCTCTGTGGA CTCTCTCTGTCTTCTATACACTCACCCCTGCTGGGGAA  
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTCTAAGCTTCACACACCCATGTACTTCTTCC  
 TCTCACACCTGGCCATCATTGACATGTCCTATGCTTCCAACAATGTTCCCAAGATGTTGGC  
 50 AAACCTAATGAACCAGAAAAGCACCATCTCCTTTGTTCCATGCATAATGCAGACTTTTTTG  
 TATTTGGCTTTTGTGTTACAGAGTGCCTGATTTTGGTGGTGATGTCCTATGATAGGTATGT  
 GGCCATCTGCCACCTTTCCAGTACACTGTCATCATGAGCTGGAGAGTGTGCACGATCCTG  
 GCCTCAACATGCTGGATAATTAGCTTTCTCATGGCTCTGGTCCATATAACTCATATTCTGAG  
 GCCGCCTTTTGTGGCCACAAAAGATCAACCACTTTATCTGTCAAATCATGTCCGTATTCA  
 55 AATTGGCCTGTGCTGGCCCTAGGCTCAACCAGGTGGTCTTATATGCGGGTTCTGCGTTTCT  
 CGTAGAGGGGCCGCTCTGCCTGGAGCTGGTCTCCAACCTGCACATCCTGTGCGCCATCTT

GAGGATCCAGTAATGGGGAGGGCCGAGACCGACTTACTCTTCCTGCTCCTTCCCACCTTT  
GCATGGTGGGACTCCTTTTTTGGCAGCACCATGGTCATGTACATGGCCCCCAAGTCCCGCCA  
CCCTGAGGAGCAGCAGAAGGTCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC  
CCCTTGATCTACAGCCTGAGGAACGCAGAGGTCAAGGGTGCCCTGAAAAGAGTGTTGTGG  
5 AAACAGAGATCAAAGTGA (SEQ ID NO: 482).

**AOLFR257 sequences:**

MESNQTWITEVILLGFQVDPALELFLFGFFLLFYSLTLMGNGIILGLIYLD SRLHTPMYVFLSHL  
AIVDMSYASSTVPKMLANLVMHKKVISFAPCIIQTFLYLAFAITECLILVMMCYDRYVAICHPL  
10 QYTLIMNWRVCTVLASTCWIFSLLALVHITLILRLPFCGPQKINHFFCQIMSVFKLACADTRLN  
QVVLFAGSFILVGPLCLVLVSYLHILVAILRIQSGEGRRKAFSTCSSHL CVVGLFFGSAIVMYM  
APKSSHSQERRKILSLFYSLFNPLNPLIYSLRNAEVKGALKRVLWKQRSM (SEQ ID NO: 483).

ATGGAAAGCAATCAGACCTGGATCACAGAAGTCATCCTGTTGGGATTCCAGGTGGACCCA  
15 GCTCTGGAGTTGTTCTCTTTGGGTTTTTCTTGCTATTCTACAGCTTAACCCTGATGGGAAA  
TGGGATTATCCTGGGGCTCATCTACTTGGACTCTAGACTGCACACACCCATGTATGTCTTC  
CTGTCACACCTGGCCATTGTGGACATGTCCTATGCCTCGAGTACTGTCCCTAAGATGCTAG  
CAAATCTTGATGCACAAAAAAGTCATCTCCTTTGCTCCTTG CATACTTCAGACTTTTTTG  
TATTTGGCGTTTGCTATTACAGAGTGTCTGATTTTGGTGATGATGTGCTATGATCGGTATG  
20 TGGCAATCTGTCAACCCCTGCAATACACCCCTATTATGAAGTGGAGAGTGTGCACTGTCCT  
GGCCTCAACTTGCTGGATATTTAGCTTTCTCTTGCTCTGGTCCATATTACTCTTATTCTGA  
GGCTGCCTTTTTGTGGCCCAAAAAGATCAACCCTTTTTCTGTCAAATCATGTCCGTATTC  
AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGTGGTCTCTATTGCGGGTTCTGCGTTCA  
TCTTAGTGGGGCCGCTCTGCCTGGTGTCTGCTCCTACTTGACATCCTGGTGGCCATCTTG  
25 AGGATCCAGTCTGGGGAGGGCCGAGAAAGGCCTTCTCTACCTGCTCCTCCACCTCTGCG  
TGGTGGGGCTTTTCTTTGGCAGCGCCATTGTATGTACATGGCCCCCAAGTCAAGCCATTC  
TCAAGAACGGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCCTGAACCCC  
CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTCCTTTGGAAA  
CAGAGATCAATGTGA (SEQ ID NO: 484).

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**AOLFR259 sequences:**

MGDNQSRVTEFILVGFLSVEMEVLLFWIFSLLYLFSLLANGMILGLICLDPRLRTPMYFFLSHL  
AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVVMYSYDRFVAICHPL  
HYTVIMNWRVCTVLAITSWACGFSLLALINLILLRLPFCGPQEVNHFFGEILSVLKLACADTWIN  
35 EIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSKEGRKKAFTSCSSHL CVVGLYFGMAMVVY  
LVPDNSQRQKQKILTLFYSLFNPLNPLIYSLRNAQVKGALYRALQKKRTM (SEQ ID NO:  
485).

ATGGGGGACAACCAATCACGGGTACAGAATTCATCCTGGTTGGATTCCAGCTCAGTGTG  
40 GAGATGGAAGTGCTCCTCTTCTGGATCTTCTCCCTGTTATATCTCTTCAGCCTGCTGGCAAA  
TGGCATGATCTTGGGGCTCATCTGTCTGGATCCCAGACTGCGCACCCCATGTACTTCTTCC  
TGTCACACTTGGCCGTCATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGCTGGA  
AAACCTAGTGAAACACAAAAAACTATCTCGTTCATCTCTTG CATTATGCAGATGGCTTTG  
TATTTGACTTTTGCTGCTGCAGTGTGCATGATTTTGGTGGTGATGTCCTATGACAGATTTGT  
45 GCGATCTGCCATCCCTG CATTACACTGTCATCATGAACTGGAGAGTGTGCACAGTACTG  
GCTATTACTTCCTGGGCATGTGGATTTTCCCTGGCCCTCATAAATCTAATTCTCCTTCTAAG  
GCTGCCCTTCTGTGGGCCCCAGGAGGTGAACCACTTCTTCGGTGAAATTCTGTCTGTCTC  
AACTGGCCTGTGCAGACACCTGGATTAATGAAATTTTGTCTTTGCTGGTGGTGTGTTTG  
TCTTAGTCGGGGCCCTTTCTCTGATGCTGATCTCCTACATGCGCATCCTCTTGGCCATCCTG  
50 AAGATCCAGTCAAAGGAGGGCCGCAAAAAGCCTTTTCCACCTGCTCCTCCACCTCTGTG  
TGGTTGGGCTTTACTTTGGCATGGCCATGGTGGTTTACCTGGTCCCAGACAACAGTCAACG  
ACAGAAGCAGCAGAAAATTCTACCCCTGTTTTACAGCCTTTTCAACCCATTGCTGAACCCC  
CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCCTTATACAGAGCACTGCAGAAA  
AAGAGGACCATGTGA (SEQ ID NO: 486).

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**AOLFR24B sequences:**

MPSINDTHFYPPFFLLLGIPGLDTHLHIWISFPFCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM  
LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQMFFIHMFTGMETVLLVVMAYDRFVAICNP  
LQYTMILTNTKISILASVVVGRNLLVTPFVFLILRLPFCGHNIVPHTYCEHRGLAGLACAPIKIN  
5 IYGLMVISYIIVDVILIASSYVLILRAVFLPSQDVRLLKAFNTCGSHVCVMLCFYTPAFFSFMTH  
RFGQNIPHYIHILLANLYVVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCTTCTATCAATGACACCCACTTCTATCCCCCTTCTTCTCCTGCTAGGAATACCAGG  
ACTGGACACTTTACATATCTGGATTCTTTCCCATCTGTATTGTGTACCTGATTGCCATTG  
10 TGGGGAATATGACCATTCTCTTTGTGATCAAACTGAACATAGTCTACACCAGCCCATTGT  
CTACTTCTGGCCATGTTGTCTATGATTGATCTGGGTCTGTCCACATCCACTATCCCCAAAA  
TGCTAGGAATCTTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT  
GTTCTTTATTACATGTTTACAGGCATGGAGACTGTTCTGTGTTGGTGGTCATGGCTTATGACC  
GCTTGTGTGCCATCTGCAACCCCTCTCCAGTACACCATGATCCTCACCAATAAAACCATCAG  
15 TATCCTAGCTTCTGTGGTTGTTGGAAGAAATTTAGTTCTTGTAAACCCATTTGTGTTTCTCA  
TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG  
TCTGGCCGGGTTGGCCTGTGCACCCATTAAGATCAACATAATCTATGGGCTCATGGTGATT  
TCTTATATTATGTGGATGTGATCTTAATTGCCTCTTCTATGTGCTTATCCTTAGAGCTGT  
TTTCGCCTTCCCTCTCAAGATGTCCGACTAAAGGCCTTCAATACCTGTGGTTCTCATGTCT  
20 GTGTTATGCTGTGCTTTTACACACCAGCATTTTTTTCTTTTATGACACATCGTTTTGGCCAA  
AACATTCCCCACTATATCCATATTCTTTTGGCTAACCTGTATGTGGTTGTCCACCTGCCCT  
TAACCCTGTCAATTTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATATTT  
GTACAGAAAGAATAA (SEQ ID NO: 488)

**AOLFR33B sequences:**

MLHTNNTQFHPSTFLVVGVPGLLEDVHVWIGFPFFAVYLTALLGNIILFVQTEQSLHQPMFYFL  
AMLAGTDLGLSTATIPKMLGIFWFNLGEIAFGACITQMYTIHICTGLESVVLTVTGIDRYIAICNP  
LRYSMILTNTKIVAILGIVHVRTLVFVTPFTFLTRLRPFVRIIPHTYCEHMGGLAKLACASINVY  
GLIAFSVGYIDISVIGFSYVQILRAVFLPAWDARLKALSTCGSHVCVMLAFYLPALFSFMTHRF  
30 GHNIPHYIHILLANLYVVVPPALNSVIYGVKTKQIREQVLRILNPKSFWHFDPKRIFHNNSVRQ  
(SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTCACCCCTCCACCTCCTCGTAGTGGGGGTCCAG  
GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCTTCTTTGCGGTGTATCTAACAGCCCT  
35 TCTAGGGAACATCATTATCCTGTTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG  
TTTACTTCTAGCCATGTTGGCCGGCACTGATCTGGGCTTGTCTACAGCAACCATCCCCA  
AGATGCTGGGAATTTTCTGGTTTAATCTTGAGAGATTGCATTTGGTGCCTGCATCACACA  
GATGTATACCATTCATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA  
GATCGCTATATTGCCATCTGCAACCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA  
40 TAGCCATTCTGGGCATAGTCATCTTGTGAGGACTTTGGTATTTGTGACTCCATTACATTT  
CTCACCCCTGAGATTGCCTTTCTGTGGTGTCCGGATTATCCCTCATACCTATTGTGAACACAT  
GGGCTTGCCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGATTGATTGCCTTCTCA  
GTGGGATACATTGACATTTCTGTGATTGGATTTTCTATGTCCAGATCCTCCGAGCTGTCTT  
CCATCTCCCAGCCTGGGATGCCCCGGCTTAAGGCACTCAGCACATGTGGCTCTCACGTCTGT  
45 GTTATGTTGGCTTTCTACCTGCCAGCCCTCTTTTCTTCTCATGACACACCGCTTTGGCCACAA  
CATCCCTCATTACATCCACATTCTTCTGGCCAATCTGTATGTGGTTTTTCCCCCTGCTCTTA  
ACTCTGTTATCTATGGGGTCAAAACAAAACAGATACGAGAGCAGGTACTTAGGATACTCA  
ACCCTAAAAGCTTTTGGCATTTTGACCCCAAGAGGATCTTCCACAACAATTACAGTTAGACA  
ATAA (SEQ ID NO: 490)

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**AOLFR112B sequences:**

MKNKTVLTEFILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILTLTLLDSHLQTPMYFFLRNFSF  
LEISFTNIFIPRVLSITTNKNSISFAGCFTQYFFAMFLGATEFYLLAAMSVDYVAICKPLHYTTI  
MSSRICIQLIFCSWLGLMAIIPITILMSQQDFCASNRLNHYFCDYEPLLELSCSDTSLIEKVFL  
55 VASVTLVVTLLVLVLSYAFIITILKLPSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKEG  
DTFNKGVALLITSVAPLLNPFYTLRNQQVKQPFKDMVKLLNL (SEQ ID NO: 491)

ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCCTGAAC  
 TCCAGGTGGCAGTTTTACCTTTCTTTTCTTGGCTATTTACTCAGCATCCTTGGAAATCTG  
 ACTATCCTCATCCTCACCTTGCTGGACTCCCACCTTCAGACTCCCATGTATTTCTTTCTCCG  
 5 GAACTTCTCCTTCTTGGAATTTCTTACAAACATCTTCATTCCAAGGGTCTGATTAGCA  
 TCACAACAGGGAACAAGAGTATCAGCTTTGCTGGCTGCTTCACTCAGTATTTCTTTGCCAT  
 GTTCCTTGGGGCTACAGAGTTTACCTTCTGGCTGCCATGTCCTATGACCGCTATGTGGCC  
 ATCTGCAAACCTCTGCATTACACCACCATCATGAGCAGCAGAATCTGCATCCAGCTGATTT  
 TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCTGATGAGTCAGCA  
 10 GGACTTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA  
 CTCTCATGTTTCAGACACAAGCCTCATAGAGAAGGTTGTCTTTCTTGTGGCATCTGTGACCC  
 TGGTGGTCACTCTGGTGCTAGTGATTCTCTCCTATGCATTATTATCAAGACTATTCTGAAG  
 CTCCCCTCTGCCCAACAAAGGACAAAAGCCTTTTCCACATGTTCTTCCCACATGATTGTCAT  
 CTCCCCTCTCTTACGGAAGCTGCATGTTTATGTACATTAATCCCTCTGCAAAAGAAGGGGAT  
 15 ACATTCAACAAGGGAGTAGCTCTACTCATTACTTCAGTTGCTCCTTTGTTGAACCCCTTTAT  
 TTACACCCTAAGGAACCAACAGGTAACCAACCCCTTCAAGGATATGGTCAAAAAGCTTCT  
 GAATCTTTAA (SEQ ID NO: 492)

**AOLFR130B sequences:**

20 MEGKNQTAPSEFIHLGFDHLNELQYLLFTIFFLTYICTLGGNVFIIVVTIADSHLHTPMYYFLGNL  
 ALIDICYTTTNVPQMMVHLLSEKKIISYGGCVTQLFAFFVVGSECLLLAAMAYDRYIAICKPLR  
 YSFIMNKALCSWLAASCWTCGFLNSVLHTVLTFLHPFCGNNQINYYFFCDIPPLLLSCGDTSLNE  
 LALLSIGILISWTPFLCILSYLYIISTILRISRSEGRHKAFSTCASHLLIVLYYGSIAITYVRPISSYS  
 LEKDRLISVLYSVVTPMLNPVIYTLRNKDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)

25 ATGGAAGGAAAGAATCAAACAGCTCCATCTGAATTCATCATCTTGGGGTTCGACCACCTGA  
 ATGAATTGCAGTATTTACTCTTCACCATCTTCTTTCTGACCTACATATGCACCTTAGGAGGC  
 AATGTTTTTATCATTGTGGTGACCATAGCTGATTCCACCTACACACACCCATGTATTATTT  
 CCTAGGAAATCTTGCCCTTATTGACATCTGCTACACTACTACTAATGTCCCCCAGATGATG  
 30 GTGCATCTTCTGTCAGAGAAGAAAATCATTTCCTATGGAGGCTGTGTGACCCAGCTCTTTG  
 CATTCATTTTCTTTGTTGGCTCAGAGTGTCTCCTCCTGGCAGCAATGGCATATGATCGATAT  
 ATTGCTATCTGTAAGCCGTTAAGGTACTCATTTATTATGAACAAGGCCCTGTGCAGCTGGT  
 TAGCAGCCTCATGCTGGACATGTGGGTTTCTCAACTCAGTGTTGCACACCGTTCTGACCTT  
 CCACCTGCCCTTCTGTGGTAACAATCAGATCAATTATTTCTTCTGTGACATACTCCCTTGC  
 35 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAAGTGGCTTTGCTGTCCATTGGGATCCTC  
 ATAAGCTGGACTCCTTTCTGTGCATCATCCTTTCTTACCTTTACATCATCTCCACCATCCT  
 GAGGATCCGTTCTCTGAGGGAGGCACAAAGCCTTTTCCACCTGTGCCTCCACCTGCTC  
 ATTGTTATTCTCTATTATGGCAGTGCTATCTTCACGTATGTGAGGCCCATCTCATCTTACTC  
 TCTAGAGAAAGATAGATTGATCTCAGTGCTGTATAGTGTTGTGACACCCATGCTGAATCCT  
 40 GTAATTTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG  
 TGGCAGCCACCAGTTTTCTCTTCTGATATATAA (SEQ ID NO: 494)

**AOLFR142B sequences:**

45 MARKDMAHINCTQATEFILVGLTDHQLKMPFLVFLSIYLFVVGNLGLILLIRADTSLNTPM  
 YFFLSNLAFFVDFCYSSVTPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLLASMAYDRY  
 VAICNPLLYMVVMTPGICIQLVAVPYSYSLMALFHTILTFRLSYCHSNIVNHFYCDDMPLRL  
 TCSDFRFLQLWIFACAGIMFISSLLIVFVSYMFIIISAILRMHSAEGRQKAFSTCGSHMLAVTIFYG  
 TLIFMYLQPSSSHALDTDKMASVFYTVIIPMLNPLIYSLQNKEVKEALKKIIINKN (SEQ ID NO:  
 495)

50 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATTCTTGTGG  
 GCCTCACAGACCATCAGGAGTTGAAGATGCCCTCTTTGTGCTATTCTTATCCATCTACCTC  
 TTCACAGTGGTAGGCAACTTGGGTTTGATCCTACTCATTAGAGCGGATACAAGTCTCAACA  
 CACCAATGTACTTCTTCTTAGCAACCTAGCTTTTGTGGATTCTGTACTCTTCTGTGATT  
 55 ACACCCAAAATGCTTGGGAATTTCTTGTACAAACAAAATGTTATATCCTTTGATGCATGTG  
 CTAATCAACTGGGCTGCTTTCTCACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG

GCCTATGACCGATATGTGGCCATTTGTAACCCTCTATTGTATATGGTTGTAATGACTCCAG  
 GAATCTGCATTCAACTTGTAGCAGTTCCTTATAGCTATAGCTTCCTAATGGCACTATTTTAC  
 ACCATCCTCACCTTCCGCCTCTCCTATTGCCACTCCAACATTGTCAACCATTTCTATTGTGA  
 TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT  
 5 GCCTGTGCTGGTATCATGTTTCATTTCTCCCTTCTGATTGTCTTTGTCTCCTACATGTTTCATC  
 ATTTCTGCCATCCTGAGGATGCATTCAGCTGAGGGAAGACAGAAGGCTTTCTCGACGTGTG  
 GCTCTCACATGCTGGCAGTCACCATATTTCTATGGGACCCTCATTTTTATGTACTTACAGCCT  
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGTCTTCTACACAGTGATCATTC  
 CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA  
 10 AAATCATTATCAATAAAAACTAG (SEQ ID NO: 496)

**AOLFR171C sequences:**

MAEVNIIYVTVFILKGITNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL  
 AFVDLCYSSAITPKMMVNFVVERNTIPFHACATQLGCFLTFMITECFLLASMA YDCYVAIC SPL  
 15 HYSTLMSRRVCIQLVAVPYIYSFLVALFHTVITFRLTYCGPNLINHFYCDDLPLALSCSDTHMK  
 EILIFAFAGFDMISSSSIVLTSYIFIIAILRIRSTQGQHKAI STCGSHMVTVTIFYGTLIFMYLPKS  
 NHSLD TDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQIL TFLKIRKLY (SEQ  
 ID NO: 497)

20 ATGGCTGAAGTTAATATCATTTATGTCAGTGTATTCTGAAAGGAATTACCAACCGGC  
 CAGAGCTTCAGGCCCCGTGCTTTGGGGTGTTTTTAGTTATCTATCTGGTCACAGTGCTGGG  
 CAATCTTGGGTTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTACTATT  
 TCCTCAGCCACCTGGCCTTTGTTGACCTTTGTTACTCCTCTGCTATTACACCGAAGATGATG  
 GTGAATTTTGTTGTGGAACGCAACACCATTCTTTCCATGCTTGTGCAACCCCAACTGGGTT  
 25 GTTTTCTCACCTTCATGATCACTGAGTGTTTCCTTCTAGCCTCCATGGCCTACGATTGCTAT  
 GTCGCCATCTGTAGTCCCCTGCATTATTCAACACTGATGTCAAGAAGAGTCTGCATTCAAC  
 TGGTGGCAGTTCCATATATATACAGCTTCCTGGTTGCCCTCTTCCACACCGTTATCACTTTC  
 CGTCTGACTTACTGTGGCCCAAACCTTAATTAACCATTCTATTGTGATGACCTCCCCTTCTT  
 AGCTCTGTCTGCTCAGACACACACATGAAGGAAATTCTGATATTTGCCTTTGCTGGCTTT  
 30 GATATGATCTCTTCTCTTCCATTGTCCTCACCTCCTACATCTTTATTATTGCCGCTATCCTA  
 AGGATCCGCTCTACTCAGGGGCAACACAAAGCCATTTCCACCTGTGGCTCCCATATGGTGA  
 CTGTCATATTTTCTATGGCACACTGATCTTTATGTACCTACAGCCCAAATCAAATCACTCC  
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGATCCCCATGTTAAACCCCC  
 TAATCTATAGTCTAAGGAACAAAGAAGTGAAAGATGCCTCAAAGAAAGCCTTGGATAAAG  
 35 GTTGTGAAAACCTACAGATATTAACATTTTAAAAATAAGAAAACCTTTATTAA (SEQ ID NO:  
 498)

**AOLFR225B sequences:**

MKNRTMFGEFILLGLTNQPELQVMIFIFLTYMLSILGNLTIITLTLDDPHLQTPMYFFLRNFSF  
 LEISFTSIFIPRLTSMITGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAICKPLHYLTI  
 40 MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFCVSNILNHYYCDYGPLVELACSDTSLLELMVI  
 LLAVVTLMVTLVLVTLSTYTIIRTLRIPSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKE  
 GGA FNKGIAVLITSVTPLLPFIYTLRNQQVKQAFKDSVKKIVKL (SEQ ID NO: 499)

45 ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCTTACAAATCAACCTGAAC  
 TCCAAGTGATGATATTCATCTTTCTGTTCTCCTCACCTACATGCTAAGTATCCTAGGAAATCTG  
 ACTATTATCACCTCACCTTACTAGACCCCCACCTCCAGACCCCCATGTATTTCTTCTCTCCG  
 GAATTTCTCCTTCTTAGAAATTTCTTTCACATCCATTTTATTCCCAGATTCTTGACCAGCA  
 TGACAACAGGAAATAAAGTTATCAGCTTTGCTGGCTGCTTGACTCAGTATTTTTTTGCTAT  
 50 ATTTCTTGGAGCTACCGAGTTTACCTCCTGGCCTCCATGTCTTATGATCGTTATGTGGCCA  
 TCTGCAAAACCCTTGCAATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACCTAGTGTT  
 CTGCTCCTGGTTGGGGGGATTCTAGCAATCTTACCACCAATCATCCTGATGACCCAGGTA  
 GATTTCTGTGTCTCCAACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGGAGCT  
 TGCCTGCTCAGACACAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTC  
 55 ATGGTTACTCTGGTGCTGGTGACACTTTCTTACACATACATTATCAGGACTATTCTGAGGA  
 TCCCTTCTGCCCAGCAAAGGACAAAGGCCTTTTCCACTTGTTCTCTCCACATGATTGTTCATC

TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAATCCTTCTGCAAAAGAAGGAGGTG  
CTTTCAACAAAGGAATAGCTGTACTCATTACTTCGGTTACTCCCTTACTGAATCCCTTCATA  
TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTCAAGGACTCAGTCAAAAAGATTGTG  
AAACTTTAA (SEQ ID NO: 500)

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**AOLFR274B sequences:**

MEFVFLAYPSCPELHLSFLGVSLVYGLIITGNILIVVSIHTETCLCTSMYYFLGSLSGIEICYTAV  
VVPFILANTLQSEKTITLLGCATQMAFFIALGSADCFLLAAMAYDRYVAICHPLQYPLLMTLTL  
CVHLVVASVISGLFLSLQLVAFIFSLPFCQAQGIEHFFCDVPPVMHVVCAQSHIHEQSVLVAAIL  
10 AIAVPFFLITTSYTFIVAALLKIHSAAGRHRAFSTCSSHLTVVLLQYGCCAFMYLCPSSSYNPKQ  
DRFISLVYTLGTPLLNPLIYALRNSEMKGAVGRVLTRNCLSQNS (SEQ ID NO: 501)

ATGGAATTTGTGTTCTCTGGCCTATCCCTCCTGCCCAGAACTGCATATTCTGTCTTCTCTGG  
GGTCAGCCTGGTTTATGGTTTGATCATCACTGGGAACATTCTCATTGTGGTGTCCATTAC  
15 ACAGAAACCTGTCTATGCACATCCATGTACTATTTCTGGGCAGCCTTTCTGGGATTGAAA  
TATGCTACACTGCAGTGGTGGTGCCCATATCCTGGCCAACACCCTACAGTCAGAGAAGAC  
CATCACTCTCCTGGGCTGTGCCACCCAGATGGCTTTCTTCATTGCACTGGGCAGTGTCTGAT  
TGCTTCCTCTTGGCTGCCATGGCCTATGACCGCTATGTGGCCATTTGCCACCCGTTGCAGTA  
CCCTCTCCTCATGACATTGACTCTTTGTGTCCACTTGGTTGTGGCATCAGTCATCAGTGGTC  
20 TGTTCCTGTCTTACAACCTGGTGGCCTTCATCTTCTCTGCCATTCTGCCAGGCTCAGGGC  
ATTGAGCACTTCTTTTGTGATGTGCCACCAGTCATGCATGTTGTTTGTGCTCAGAGTCACAT  
TCATGAGCAGTCAGTGTCTGGTGGCAGCCATACTAGCCATTGCTGTGCCTTTCTTCCTCATC  
ACCACCTCCTACACCTTCATAGTGGCTGCTCTGCTCAAGATCCACTCGGCTGCTGGCCGCC  
ACCGGGCCTTCTCCACCTGCTCTTCCCACCTCACTGTGGTGTGCTGCTGCAGTATGGCTGTGT  
25 GCCTTCATGTACCTGTGCCCCAGCTCCAGCTACAACCCCAAGCAAGATCGGTTTCATCTCAC  
TGGTGTACACATTGGGAACCCCACTGCTCAACCCACTTATCTATGCCCTGAGGAACAGTGA  
GATGAAAGGGGCCGTAGGGAGAGTTCTTACCAGGAAGTGCCTTTCCAGAACAGCTAG  
(SEQ ID NO: 502)

**AOLFR276B sequences:**

MGGFGTNISSSTSFTLTGFPEMKGLEHWLAALLLLLYAISFLGNILILFIKKEEQLHQPMYYFLS  
LFSVNDLGVSFSTLPTVLAAVCFHAPETTFDACLAQMFFIHFSSWTEFGILLAMSFHDHYVAICNP  
LRYATVLTDRVAHNGISIVIRSFVPLPFLKRLPFCKASVVLASVCLHADLRLPWGDT  
TINSMYGLFIVISAFGVDSLILLSYVLILHSVLAIASRGERLKLNTCVSHIYAVLIFYVPMVSVS  
35 MVHRFGRHAPEYVHKFMSLCTSNALPNYLFHQD (SEQ ID NO: 503)

ATGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG  
AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGCTGCTGCTTTATGCTATTTCTT  
CCTGGGCAACATCCTCATCCTCTTTATCATAAAGGAAGAGCAGAGCTTGCACCAGCCAATG  
40 TACTACTTCTGTCTCTTTTTCTGTTAATGACCTGGGTGTGCTCTTTCTACATTGCCCACT  
GTACTGGCTGCTGTGTGTTTCATGCCCCAGAGACAACCTTTGATGCCTGCCTGGCCCAGA  
TGTTCTTCATCCACTTTTCTCCTGGACAGAGTTTGGCATCCTACTGGCCATGAGTTTGAC  
CACTATGTGGCCATCTGTAACCCGCTGCGCTATGCCACAGTGCTCACTGATGTCCGTGTGG  
CCCACAATGGCATATCCATTGTATCCGAGCTTCTGCATGGTATTTCCCACTTCCCTTCTC  
45 CTGAAGAGACTGCCTTTCTGTAAGGCCAGTGTGGTACTGGCCATTCTACTGTCTGCATG  
CAGACCTGATTTCGGCTGCCCTGGGAGAGACTACCATCAACAGCATGTATGGCCTGTTTAT  
TGTCATCTCTGCCTTTGGTGTAGATTCACTGCTCATCCTCCTCTCCTATGTGCTCATTCTAC  
ATTCTGTGCTGGCCATTGCCTCCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTGTC  
ACATATCTATGCAGTGCTGATCTTCTATGTGCCTATGGTTAGTGTGTCCATGGTTTCATCGAT  
50 TTGGGAGGCATGCTCCTGAATATGTGCACAAGTTCATGTCTCTTTGTACCTCCAATGCTCT  
ACCAATTATCTATTCCATCAAGACTAA (SEQ ID NO: 504)

**AOLFR311B sequences:**

MDWENCSSLTDFFLLGITNNPEMKVTLFAVFLAVYIINFANLGMIVLIRMDYQLHTPMYFFLS  
55 HLSFCDLCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLLSVMAFDYKAIINP  
LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFRLCFCGSNEINHFFCDIPLLLLSRSDTQV



NELVLFTVFGFIELSTISGVFISYCYIILSVLEIHS AEGRFKALSTCTSHLSAVAIFQGTLLFMYFRP  
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKEALKKLKNKILF (SEQ ID NO: 505)

5 ATGGACTGGGAAAATTGCTCCTCATTAAGTATTTTTTCTCTTGGGAATTACCAATAACCC  
AGAGATGAAAGTGACCCATTTGCTGTATTCTTGGCTGTTTATATCATTAATTTCTCAGCAA  
ATCTTGGGAATGATAGTTTTAATCAGAATGGATTACCAACTTCACACACCAATGTATTTCTT  
CCTCAGTCATCTGTCTTTCTGTGATCTCTGCTATTCTACTGCAACTGGGCCCCAAGATGCTGG  
TAGATCTACTTGCCAAGAACAAGTCAATACCCCTCTATGGCTGTGCTCTGCAATTCTTGGT  
CTTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTCAGTGATGGCCTTTGATCGGTACA  
10 AGGCCATCATCAACCCCCTGCTCTATACAGTCAACATGTCTAGCAGAGTGTGCTATCTACT  
CTTGAAGTGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC  
CGCCTATGCTTCTGTGGGTCTAATGAGATTAATCATTCTTCTGTGATATCCCTCCTCTCTT  
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTAGTGTTATTACCGTCTTTGGTTTTA  
TTGAAGTGAAGTACCATTTTCAAGAGTTTTTCAATTTCTTATTGTTATATCATCCTATCAGTCTTG  
15 GAGATACACTGCTGAGGGGAGGTTCAAAGCTCTCTACATGCACTTCCCACCTTATCTG  
CGGTTGCAATTTTCCAGGGAACCTGCTCTTTATGTATTTCCGCGCAAGTTCTTCTATCT  
CTAGATCAAGATAAAATGACCTCATTGTTTTACACCCTTGTTGGTCCCATGTTGAACCCCCT  
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAACTGAAAAATAAAAT  
TTTATTTTAA (SEQ ID NO: 506)

20

**AOLFR314 sequences:**

MEVKNCCMVTEFILLGIPHTEGLEMTLFLVFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG  
NLSVFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFFHFLGSIECFLFTVMAYDRFTAICY  
PLRYTVIMNPRICVALAVGTWLLGCIHSSILTSFTFLPYCGPNEVDHFFCDIPALLPLACADTSL  
25 AQRVSFTNVGLISLVCFLILLSYTRITISILSIRTTEGRRRAFSTCSAHLIAILCAYGPIITVYLQPT  
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKTALKTILHRTGHVPES (SEQ ID NO: 507)

30 ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTCATCCTTTTGGGAATCCCACACACA  
GAGGGGCTGGAGATGACACTTTTTGTCTTATTCTTGCCCTTCTATGCCTGCACTCTACTGGG  
AAATGTGTCTATCCTTGTGCTGTTATGTCTTCTGCTCGCCTTCACACACCTATGTATTTCT  
TCCTGGGAAACTTGTCTGTGTTTGACATGGGTTTCTCCTCAGTGACTTGCCAAAATGCT  
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT  
TCTTCCATTTCTCGGGAGCATTGAGTGCTTCTTGTTTACGGTGATGGCCTATGACCGCTTC  
ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC  
35 TGGCTGTGGGCACATGGCTGTTAGGGTGCATTCATTCCAGTATCTTGACCTCCCTCACCTTC  
ACCTTGCCATACTGTGGTCCCAATGAAGTGGATCACTTCTTCTGTGACATTCCAGCACTGTT  
GCCCTTGGCCTGTGCTGACACATCCTTAGCCCCAGAGGGTGAGCTTCACCAACGTTGGCCTC  
ATATCTCTTGTCTGCTTTCTGCTAATTTTATCCTACACTAGAATCACAATATCTATCTT  
AAGCATCTGACAACTGAGGGCCGTGCGCTTCTCCACCTGCACTGCTCACCTCATCTATT  
40 GCCATCCTCTGTGCCTATGGGCCCATCATCACTGTCTACCTGCAGCCACACCCCAACCCCA  
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCCCTTGAT  
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAACAATATTGCACAGGACAGG  
CCATGTTCTCTGAGAGTTAG (SEQ ID NO: 508)

45 **AOLFR324B sequences:**

MPIANDTQFHTSSFLLLGIPGLEDVHIWIGFPFFSVYLIALLGNAAIFFVIQTEQSLHEPMYCYLA  
MLDSIDLSTATIPKMLGIFWFNIKEISFGGYLSQMFFIHFFTVMESIVLVAMAFDRYIAICKPL  
WYTMILTSKIISLIAGIAVLRSLYMPIVFLVLLRPLFCGHRIPHTYCEHMGIA RLACASIKVNIM  
FGLGSISLILLDLVLLIILSHIRILYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH  
50 DIPQYIHIFLANLYVVVPPTLNPIYIGVVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCATACTTCTTCATTCCCTACTGCTGGGTATCCCAGG  
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTTTTCTCTGTGTATCTTATTGCACTCC  
TGGGAAATGCTGCTATCTTCTTTGTGATCCAACTGAGCAGAGTCTCCATGAGCCCATGTA  
55 CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTGTCTACGGCCACCATTCCCAAA  
ATGCTGGGCATCTTCTGGTTCAATATCAAGGAAATATCTTTTGGAGGCTACCTTTCTCAGA

TGTTCTTCATCCATTTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC  
 CGCTACATTGCCATTTGCAAACCTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA  
 GCCTCATTGCAGGCATTGCTGTCCTGAGGAGCTTGACATGGTCATTCCACTGGTGTCTTCT  
 CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG  
 5 GCATTGCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT  
 TTCTCTCTTGTATTGGATGTGCTCCTTATTATTCTCTCCCATATCAGGATCCTCTATGCTGT  
 CTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT  
 GGTGTTATCTTAGCCTTTTCTACACCAGCATTTTCTCTTTCTTTACACACTGCTTTGGCCAT  
 GATATCCCCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTTGTTCCCTCCCACCT  
 10 CAATCCTGTAATCTATGGGGTCAGAACCAACATATTAGGGAGACAGTGCTGAGGATTTTC  
 TTCAAGACAGATCACTAA (SEQ ID NO: 510)

**AOLFR328 sequences:**

15 MALGNHSTITEFLLGLSADPNIRALLFVLFGLGIYLLTIMENLMLLLVRADSCLHKPMYFFLSH  
 LSFVDLCFSSVIVPKMLENLLSQRKTISVEGCLAQVFFVFTAGTEACLLSGMAYDRHAAIRRP  
 LLYGQIMGKQLYMHVWGSWGLGFLDALINVLLAVNMVFCEAKIIHHYSYEMPSLLPLSCSDI  
 SRSLIVLLCSTLLHGLGNFLLVFLSYTRIISTILSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL  
 MPNSGSPIELIFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGCACCATCACCGAGTTCCTCCTCCTTGGGCTGTCTGCCGACC  
 CCAACATCCGGGCTCTGCTCTTTGTGCTGTTCTTGGGATTACCTCCTGACCATAATGGA  
 AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGTCTCCATAAGCCCATGTATTTCT  
 TCCTGAGTCACCTCTCTTTTGTGATCTCTGCTTCTCTTCAGTCATTGTGCCCAAGATGCTG  
 GAGAACCTCCTGTACAGAGGAAAACCATTTAGTAGAGGGCTGCCTGGCTCAGGTCTTCT  
 25 TTGTGTTTGTCACTGCAGGGACTGAAGCCTGCCTTCTCTCAGGGATGGCCTATGACCGCCA  
 TGCTGCCATCCGCCGCCACTACTTTATGGACAGATCATGGGTAAACAGCTGTATATGCAC  
 CTTGTGTGGGGCTCATGGGGACTGGGCTTTCTGGACGCACTCATCAATGTCCTCCTAGCTG  
 TAAACATGGTCTTTTGTGAAGCCAAAATCATTCACTACAGCTATGAGATGCCATCCCT  
 CCTCCCTCTGTCCTGCTCTGATATCTCCAGAAGCCTCATCGTTTTGCTCTGCTCCACTCTCC  
 30 TACATGGGCTGGGAACTTCCTTTTGGTCTTCTTATCCTACACCCGTATAATCTCTACCATC  
 CTAAGCATCAGCTCTACCTCGGGCAGAAGCAAGGCCTTCTCCACCTGCTCTGCCCACCTCA  
 CTGCAGTGACACTTTACTATGGCTCAGGTTTGTCTCCGCCATCTCATGCCAACTCAGGTTTC  
 CCCCATAGAGTTGATCTTCTCTGTGCAGTATACTGTAGTCACTCCCATGCTGAATTCCCTCA  
 TCTATAGCCTGAAAAATAAGGAAGTGAAGGTAGCTCTGAAAAGAACTTTGGAAAAATATT  
 35 TGCAATATACCAGACGTTGA (SEQ ID NO: 512)